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FIGURE 173

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTGAAGGTCTAGCCCACCTGGGCTGGCTC
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCGGACTCTGTCGTCGTTAAGGCCACTCC
TATTCTACGGCTGACCCCTGGTGGTACGTGGATCTGTCGCCACGCAAGTCTGGGTCTTCG
GCGATTGACCAGGGGTCTTGCTGTTGGGAGCCTCTCCTAACGCTGCCTGTTCGCGCAGAGTT
TGGAGGGGCGGGTTGGGTCGGTGTCTGATTGGGCTCGCACCGCAGCACGCTGGAGTCCCG
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTCAAGCGGTGCCGGACACCCGTGTGG
CAGGCGCGAAGCGCTCTGGAGAAATCCCAGCAGCCCTGCTCCCTGCAGCCAGGTGTAGTT
GGGAGCCACTGGGCCAAAGTGAGAGTCCAGCGGTCTCCAGCGCTTGGCCACGGCGCGGC
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGTTGGCTGGCC
TGCTCTGGGGCCCTGCTGGAAACGCCCTGGCTGGAGGCCAGGATCTCCACTGTGGAG
CATGCAGGGCTCTGGTGGATGAACATAGAACATGGAAATTGCCAGGTGGACCCAAAGAACCA
TTCAGATGGATCTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG
CCCGCTCAGAGGCCACCTCACAGAGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG
GGAACAGATTGATCCTCACCCATCGCAAGAACTACGTACGTGTAGTGGCCGAATGGAG
AATCCAGTGAACCTGGACCTACAAGGCATCGAACCGACTCAGATATTAGCGGCACCCCTCAAGT
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTCCCAGGAGG
CTGACAATGTTAAAGACAAACTTGCAGTAAGCGAACAGATCTTGTGACCATGCCCTGCACA
TATCGCATGATGAGCTTGAACCACTGGAGCAGCCACACTGGCTTGATGGATCACCCCCAGG
AGGGAAAATGGTGGCAATGCCTTTATATATTATGTTTACTGAAATTAACTGAAAAATA
TGAAACCAAAAGT

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FIGURE 174

MKGWGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKTIQMGSFRINPDGS
QSVVEVPYARSEAHLEELEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRID
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTLCDHALHISHDEL

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 12-18, 16-22, 29-35

Endoplasmic reticulum targeting sequence.

amino acids 179-184

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FIGURE 175

CGCAGCGCGGAGTCCTGATGGCCGGCATGGTTACCGCTGCTGCCCTGCTGTCCTCG
GTCGGCGCGTGGCTAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAACTGCAGGGTGGG
AGATTCTGATGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG
ACAGTGAAACCCCTTGCCATCGACATATTCTGTCACCAACAAAGATTCAGGGATTTGTC
AGGGAGAAAAGTATCGGACAGAAGCTGAGATGTTGGATGGAGCTTGTCTTGAGGACTTT
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA
GTGGAAAAGGCATTTGGAGGCAGCCTGCAGGTCTGGCTTGGCATCCGAGAGAGACTGGAG
CACCCAGTGTACACGTGAGCTGGAATGACGCCGTGCCTACTGTGCTTGGCGGGAAAACGA
CTGCCACGGAGGAAGAGTGGAGTTGCCGCCAGGGGCTGAAGGGTCAAGTTACCCA
TGGGGAACTGGTCCAGCAAACCGCACCAACCTGTGGCAGGGAAAGTCCCCAAGGGAGAC
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTCCCCGCCAGAACAACTAC
GGGCTCTATGACCTCCTGGGAACGTGTGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG
CAGGACATGCGCGTCCTCCGGGGGCATCCTGGATCGACACAGCTGATGGCTTGCAATCAC
CGGGCCCGGGTCAACCACCAGGATGGCAACACTCCAGATTCAGCCTCAGACAACCTCGGTTTC
CGCTGTGCTGCAGACGCAGGCCGCCAGGGAGCTGTAAAGCAGCCGGTGGTACAAGGA
GAAAAGCCTCTAGGGTCACTGTCATTCCCTGGCATGTTGCAAACAGCGCAATTCAAGCTC
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCTCCCTGTCTCCATCCCTGTGTCAGGCGC
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTGGAGAAGGGCCAATGTGTGTT
GACGATGGCTGGGGCCAGGTGTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAA
CACACAAACAGTTGAACAGAGCACTCTGAAAGGCCATTAAGCAATTAAATCTATTC
TCTCCCCTTCTCCCTGGATGATTCAGGAAGCTGACATTGTTCTCAAGGCAGAATTTC
TGGTCTGTTCTCAGCCAGTGCTGTGGAAGGAGAATGCTTCTTGCGCTCATCTGTG
GTTCTGTCCTCTGAAGGAAACTAGTTCACTGTGTAACAGGCAGACATGTAACTATTAA
AAGCACAGTTCAGTCTAAAGGGTCTGGAGAACCCAGATGATGACTAGGTGAAGCATTGCA
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTCCTATTCTT
TTTTTTTTTTTTTTGAGACAGGGTCTTCTGTTGCCAGGCTAGAGTGCACTG
TGATCACGGCTCACTCTAGCCTGAATTCCCTGGGCCAAGCAATTCTCCCACCTCAGCCTCC
TGAGTAGCTGGACTACAAGTGTGACCACCATGCCCTGGCTAATTGTTGAATTGTTGAGTG
ATGGGATCTCGCTCTGTTGCCAGGGTGGCTCGAACTCCTGGCTCAAGCGATCCTCCCACC
TCGACCTCCAAAGTGTGGATTACAGGTGTGAGCCACCTCGCCTGGCCCCCTCTCCATA
TGCCCTCAAAACATGTCCCTGGAGAGTAGCCTGCTCCCACACTGTCACTGGATGTCATGGGG
CCAATAAAATCTCCTGCAATTGTTGATCTCAAAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 176

MARHGLPLLPILLSLLVGAWLKLGNQATSMVQLQGGRFLMGTNSPDSRDGEGPVREATVKPFA
IDIFPVTKDFRDFVREKKYRTEAEMFGWSFVFEDFVSDELRNKATQPMKSVLWWLPVEKAFW
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ
PNRTNLWQGKFPKGDKAEDGFHGVPVNAFPQAQNNYGLYDLLGNVWEWTASPYQAAEQDMRVL
RGASWIDTADGSANHRARVTTRMGNTPDSASDNLGFRCAADAGRPPGEL

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 191-195

N-myristoylation sites.

amino acids 23-29, 25-31, 175-181

Amidation site.

amino acids 159-163

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FIGURE 177

GCCTCTCGCCCTGACCATGCACCCCTGCATCTCCTGCTGGGCCACAGGCAGCGCTTAT
TTCTGGAGCTGAGGGCTAAAACTTTTGACTTTCTCCTCAACATCTGAATC**ATGCCAT**
GTGCCAGAGGAGCTGGCTTGCAAACCTTCCGTGGCTCAGCTCCTTAACTTGGGCGC
TTTGCTATGGAGACAGCCTCAGCCAGGCCGGTCGCTTCCGGACAGGAGGCAAGAGCATT
TTATCAAGGGCTGCCAGAATACCACGTGGTGGTCCAGTCCGAGTAGATGCCAGTGGCATT
TTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTGGATGGCT
CAGAGGACTGGGTGTACTACAGAATTCTCACGAGGAGAAGGACCTGTTTTAACTTGACGG
TCAATCAAGGATTCTTCCAATAGCTACATCATGGAGAAGAGATATGGAACCTCTCCATG
TTAAGATGATGGCTTCCCTGCCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTCTACAGCAGGGCA
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTCCAACCTACAC
ATGGAGACTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCGC
ACATCGTTACAGGAGGCAGAAAGTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA
TTGTGACTCACATGTCCTCTGGTTGAAGAATCTGTTGTTGG**TAG**TTTATTAAA
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTAAATATCTCA
TGACATTCAAATCTCTCTGTATTCTGCCAGAAAGTGTACATTCTTTGCTGTATAAA
CCCTTCACTTGTC

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FIGURE 178

MPCAQRSLANLSVVAQLLNFGALCYGRQPQPGPVRFDRRQEHIKGLPEYHVVGPVRVDAS
GHFLSYGLHYPISSRRKRDLDGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL
SHVKMMASSAPLCHLSGTVLQQGTRVGAALSACHGLTGFFQLPHGDFFIEPVKKHPLVEGGY
PHPHIVYRRQKV PETKEPTCGLKGIVTHMSSWVEESVLFFW

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 11-15, 105-109, 125-129

N-myristoylation site.

amino acids 149-155

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FIGURE 179

CAGATTAAAAAGAAAACTTACTGAATCAGCTGAGTGTAAATAATACGAATTCCCTTCT
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGAT**ATGTGTGGATTACAGTTTCTCT**
GCCTGCCTACGACTGTTCTGGTTACCTGTTATCTTTATTATTACTCCACAAAGAAAT
ACTTGGATGTCGTCTGTTGTCAGCTGCAGCTGGGAGACAAATTAACTGCCGTAACTTAGG
CCTTCGAGTATTCCCTAAGAATTTCCTGAAAGTACAGTTCTGTATCTGACTGGGAATAA
TATATCTTATATAATGAAAGTGAATTAAACAGGACTTCATTCTCTTGTAGCATTGTATTTGGA
TAATTCTAACATTCTGTATGTATATCCAAAAGCCTTGTCAATTGAGGCATCTATATTTCT
ATTTCTAAATAATAATTTCATCAAACGCTAGATCCTGGAATTAAAGGGACTTTAAATCT
TCGTAATTATTTACAGTATAATCAGGTATCTTGTGAGAGGAGTATTAAATGATCT
AGTTTCAGTTCACTAAATCTACAAAGGAATGCCCTCACTGTCCTGGGAGTGGTACCTT
TGTTGGTATGGTGCTCTCGGATACTTGATTTATCAAACAATAACATTGAGGATATCAGA
ATCAGGCTTCAACATCTGAAAACCTTGCTTGTATTAGGAAGTAATAATTAAACAAA
AGTACCATCAAATGCCCTTGAAGTACTTAAAGTCTAGAAGACTTCTTGTCTCATAATCC
TATTGAAGCAATAACAGCCCTTGCATTAAAGGACTTGCCTGGAATACCTCCCTGAA
AAATTCAAGAATTAGGAATGTTACTAGGGATGGGTTAGTGGAAATTAAATCTAAACATT
GATCTTAAGTCATAATGATTAGAGAATTAAATTCTGACACATTCACTTGTAAAGAATT
AATTACCTTAAGTTAGATAGAACAGAATAATTAGCATTGATAATGATACTTGTAAAATAT
GGGAGCATCTTGAAGATCCTTAATCTGTCATTAAATCTACAGCCTGCACTAACAGGGT
CCTTAAGCCGTTGTCTTCATTGATTCACTTCAGGCAAATTCTAATCCTGGGAAATGTAAC
CAAACTTTGGCCTTCGAGACTGGCTAGCATCTCAGCATTACTCTAAACATCTATTGTC
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAAACATTACAAATTGTGTTAC
TTCAATAATGTATCCAGAGCTGGCTGTTAAAATCTCTCATATTCAACAGACTAC
TGCCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC
TGAGAACATTACTTCTGGAACGAATTCTACTTCACCTGCTGGTAGATTTCAAGAGAA
TGCCTTGGTAATCCATTAGAGACTACAGCAGTGTACCTGTGCAAATACAACATTACTTC
TGTTACCTGAACCTGGAAAAAACAGTGCCTACCGAATGATGCTGCTCAATGTCAGGGAA
AACATCTCTAATTGTCACACAAGAAGTTGAGAAGTTGAATGAGGCTTTGACATTTGCTAGC
TTTTTCATCTTAGCTGTGTTAATCATTGATCTACAAAGTTGTCAGTTAAACA
AAAACCTAAAGGCATCAGAAAACCTCAAGGGAAAATAGACTTGAATACTACAGCTTTATCAGTC
AGCAAGGTATAATGTAACGCCTCAATTGTAACACTTCCCAAATTCTCTAGAAAGTCCCTGG
CTTGGAGCAGATCGACTTCATAAACAAATTGTCCTGAAAATGAGGCACAGGTCATTCTTT
TGAACATTCTGCTTA**TAA**CTCAACTAAATATTGTCATAAGAAAATTCACTGTCATTG
GATTAAACTGAAACCTCCTATATAATTATACCTTAGTTGGAAATATAATGAATTATATG
AGGTTAGCATTATAAAATGTTTTNTAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 180

MCGLQFSLPCILRLFLVVTCYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTV
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLQRNRLLTVLGSHTFVGMVALRILDLSN
NNILRISESFGHQHLENLACLYLGSSNLTKVPSNAFEVLKSLRRRLSLSHNPIEAIQPFAFKGLA
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYLKLDRNRIISI
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSIHLQANSNPWECKNCCKLLGLRDWLASSA
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRRAWVKSPHIHHKTALMMAWHKVTNG
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTLNLEKNSALPN
DAASMSGKTSЛИCTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL
EYYSFYQSARYNVTASICNTSPNSLESPGLEQIRLHKQIVPENEAQVILFEHSAL

Signal peptide:

amino acids 1-41

Transmembrane domain:

amino acids 530-547

N-glycosylation sites.amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

N-myristoylation sites.

amino acids 3-9, 69-75, 126-132, 174-180

ATP/GTP-binding site motif A (P-loop).

amino acids 506-514

FIGURE 181

GGCCTGGCGCGCGCTCCGTAAGCGTGTGCGGCAGGGCGGGACAGAACCGTCCTCTCG
GGCTCTGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG
GCATTGTCCCCCCTGGCACAGTTGGCCTTTCCAGAAGCCCCTTGTGTTACGTCT
AAATTGCGTCGGTTCTTATTCTCTCCCTGGCAAGGTCTGAAGACGGTAGGAGAATAACCT
GTGTCAGCGTGT ATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT
GAAATATTCAAGGCTCTCCAGCACAGCATGGCTACATTGACCTTCAGTTAAGAAAACCCC
TCCTAACGATCCCTTATAAGGCCATCGCACTGCCACTGTGCTGTTTGATTGGCGCCTTCT
CATTATTATAGGCTCCCTCCTGCTGTCAGGCTACATCAGCAAAGGGGGGCAGACCGGGCGT
TCCAGTGCTGATCATTGGCATTCTGGTGTTCCTACCCGGATTTACCACCTGCGCATCGCTTA
CTATGCATCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTGATGACT TAGCA
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAACTGTCCAGCTTAAGATATCTAGCAGAA
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTGCAGATGTTAAGAAAATAATGCCAGATT
TTTGGGTCTTCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT
TTTCATCCCTGGGCCCTGACAAGTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA
TTCTGTAATGAAAAGTGTGCCTGCCACCACCCCTGTAGAGCTGAGCATTCTTTAAATA
GTCTTCATTGCCAATTGTTCTGTAGCAAATGGAACAATGTGGTATGGCTAATTCTTATTA
TTAAGTAGTTATTTAAAAATCTGAGTATATTACCTGTACACTTATCCCTACCTTCATG
TTCCAGTGGAAAGACCTTAGTAAATCAAAGATCAGTGAGTCATCTGTAATATTTTTACT
TGCTTCTTACTGACAGCAACCAGGAATTTTATCCTGCAGAGCAAGTTCAAAATGTA
ATACTCCTCTGTTAACAGTCCTGGACCATTCTGATCCAGTTCAACAGTAGGTTGGACAGC
ATATAATTGATCATTGTCCTGTAAATCAAGATGTTCTGCAGATTATCCTTTAACGG
CCGGACTTTGGCTTTCTAATGAAACATGTAGTGGTTATTATTTAGAGTTATAGCCGTA
TTGCTAGCACCTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCC
AGAGGACTAGATCACCTAGTTGATTCTATTAGCTGCAAAAGTGACTTATATTCCA
AAGAAATTAAAATGTTGAAATCCAAATCCTAGAAATAAAATGAGTTNNNTCCAAAAAA
AAA

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FIGURE 182

MMPSRTNLATGIPSSKVYSRLSSTDDGYIDLQFKKTPPKIPIYKAIALATVLFLIGAFLIIIG
SLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

Transmembrane domains:

amino acids 45-66, 79-95

N-myristoylation sites.

amino acids 11-17, 75-81

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FIGURE 183

CTAAAAAAATACAAAATTAGCTGGCGTGGTGTATGTACCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA
GAATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAGTCAGTCACCTCCAGCCTGGGTGACAGA
GCAAGACTCTGTATCAAATAAATAAAATAAAAGTACAACCTCTGGATGGGATGGTGGCTTATGTCGTATGCCAG
CACTTGGGAACTTGAGGCGGGTAGATTGCTTGAGTCCGGAGTTGAGACAGTCTGGTAATATGGTAACCT
GTCTACCAAAATACAGGTATTAGCCAGTCTCATAACTCGGCTCTAAAATAAAATACATACATAGATG
AAAATTAAAAAATAAAAGTCCAACTCAGCGGTTTCAGCATATTCAGAGTTGACATCTTCACCACTATCTA
ATTCAGAACATTTCATCCCCAAAAGAAACCTAACCCATTGACTATCTCTCCATTCCTCCCTCCCTAG
CCTCTGGCAACCACAACTATCTTTTGTCTATAGATTGCTATTTGGACAGTCACTACAGGAATCAT
ACCACATGTAGCCTTTGTGTCGGCTCTTGATTAATAGAATGTTCAAGGCTCATCTATGCTGTAGCCTGT
ATCAGCACTCATTCTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTCCACTAGCTGAT
GGACATTGGGTTGTTCCACCTCTGGCTATTATAATATTGCTGCTATAAATATTCACTACAAGTTTGTG
TGGACATATGTTTATTCCTGGTATATCCTCGGAGTGAACGTGCTGGATCAGTGGTAACTCTAGGTCTA
ACCTGGCAGTTAACAGAACCTATGCATGCTGTAGTCCATGAGTTGAAATAAACACTTGACCCATAGTAAGTGC
CAGATCATCTTCATTTCACAGCAACCAGTAATTTCACAGATGAGGAATGAAGGCTCCAGAGGTGAACCTGGCTT
TTCCCATTTGAGCAGTTCCAAGTCAGACAGTTAAAAGTGGCAGGACCTGGAAGAGAAGCTAGTTCTTCCACCT
GGCATTCAAGGCTGCCTCTGGCTACGGGCTGGCATTTAGAATAGAGCTAACGGTCTGCTGCCAAGGCAAGGTGC
CCCAGTCTGCCTCTCTGTGCTTATTCCACTTTCTGCAAGCCCTCCAGGGGACCCCTCTCAGCCACCCCTC
TCTCTGGTGA~~TG~~TCACAGTGTGCTGCCAGAGATCAAAGATAACGGTGCAGAAACTGGCTCGGACCATAAAGGACATT
CACAGCAGTGTATCCGAGTGGCAAAGCCATTGACAGGAACCTCGACTCTGAGATCTGTTGTTGTCAGAT
GCGGTGTTGGGACCCGGGAAACAGCAGCAGCAGATGGCAGTGGCAACCTGTATCAGCAGGGC
ATGCTCAGCGTGGCCAGGGAGCTGTGCGCAGGAATCAACGCTGAATGTGGACTTGGATTTCAGCAGCCTTCTA
GAGTTGAATCGAATCCTGGAAAGCCCTGCAAGAACAAAGACCTGGCTCTGCGTTGGATGGCCGCTCCCACAGG
CAGCGCCTGCTGGAACTCAACAGCTCCCTGGAGTTCAAGCTGCACCGACTGCACTTCATCCGCTCTGGCAGGA
GGCCCCCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACTCCAGCCCTTGCTCGGCTGCACCGAGGGAG
ATCCAGGTGATGGCAGCCTGGTGTACCTGCGGCTGGGCTTGGAGAAGTCACCCACTGCCCCACTGCTGGAC
AGCAGCCACTGGCAGAGATCTGTGAGACCTTACCCGGGACGCCCTGTCCTGCTGGGCTTCTGTTGAGTCC
CCCCTAGCGTCAGTTGCTCTGGCTGTGTCGGCTGCGCTGTGATGAACATCAAGGCTGTGATTGAGCAG
CGGCAGTGCAGCTGGGCTGGAATCACAAGGACGAGTTACCGATTGAGATTGAACTAGGCATGAAGTGTGGTAC
GCTCATCTGTGGCCATGTTATCTCCGAGATGCACTCAATAAGCTATTAATGGAGGAAACACTCCGTGTTGCT
TGCCCCATCCTCCGCCAGCAGCTCAGATTCAACCCCTCCATCAAGCTGAAGTGTCCCTACTGTCCCATGGAG
CAGAACCCGGCAGATGGAAACGCATCATATTCT~~TG~~ATTCTACCTGGAGGAATTGGTGTGAAAGGGGTTTCAC
CTGTGAGCCTGGTCTGTCTGGTAGGGTGGTCAACTCAGTGGACTGTGGTTGGTTCAGAGCCCTGGCTGAG
GAGTTCCACTGAGGGGAGCAGTGGAGCAGCCCTTGGCAGAGGCTGAGGAGGAGATGGACCCAGGCCCCACGCC
CACCTGGCTCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTGTCTTCTGTTCTGTTGC
GTTTGACTTAGCAACCGACAGGTGGCAAGGGATTGGCTTCAGCAGTAGACATCCTCCACCCCTGCC
CAGCCAAGTCTCTGCTGCCATGCCAATGCTATGTCACCCCTGCCAGGGCCAAGAGTGTCCAGCGGTGGCC
CACCTCTCCCTCCACTACAGCCTCAACAGTATGTAACCATCTCCACTGTAATAGTCCCAGTTAGAACGGAATG
CCGTTGTTTATAACTTGAACAAATGTATTACTGCCCTCTCAAAA

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FIGURE 184

QCCRKIKDTVQKLASDHKDIHSSVSRRVGKAIDRNFSEICGVVSDAVWDAREQQQQILQMAIV
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRIALHEQDLGPALEWAVSHRQLLEL
NSSLEFKLHRLHFIRLLAGGPALKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRGLEKSP
YCHLLDSSHWAECETFTRDACSLLGLSVESPLSVFASGCVALPVLNMNIKAVIEQRQCTGVW
NHKDELPPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLICGHVISRDALNKLINGGKLKCP
YCPMEQN PADGKRIIF

Transmembrane domain:

amino acids 222-241

N-glycosylation site.

amino acids 129-133

Tyrosine kinase phosphorylation site.

amino acids 151-159, 184-193

Amidation site.

amino acids 327-331

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 222-233

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FIGURE 185

GAGCGACGCTGTCTTAGTCGCTGATCCAAATGCACCGGCTCATTTGTCTACACTCTAAT
CTGCGCAAACCTTTCAGCTGTCGGGACACTCTGCAACCCCGCAGAGCGCATCCATCAAAGC
TTTGCAGCAACGCCAACCTCAGGGAGATGACTTGACCGAAGAGATGAGACCATTCCAGGTGAA
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAGGAACCTGCTCCTGAC
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGACAATCAGTTGGATT
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTGTGGAAGTTGAAGATATATCCGAAAC
CAGTACCAATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCCTCCAAGGATAAAATCAAG
AACGAACCAAATTAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAACCTGGATTCAA
GATTATTATTCTTGCTGGAAGATTCCAACCCGCAGCAGCTCAGAGACCAACTGGGAATC
TGTCAAGCTCTATTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCACTCTGAT
TGCAGGATGCTCTGGACAAAAAAATTGCAGAATTGATACTGAGATCTGCTCAAGTACTT
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG
CAGGTCAACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCAATGT
GGTCTTCTTCCACGTTGCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACGT
CAACTGGAGGTCTGCACATGCAATTCAAGGGAAAACCGTGAAGGAAATTGTGAGGTATTACA
GTTGAGCCTGCCACATCAAGAGGAGGGTAGAGCTAAGACCATGGCTTAGTTGACATCCA
GTTGGATCACCAGTGAACGATGCGATTGTATCTGCAGCTCAAGACCACTCGATAAGGAGAATGT
GCACATCCTTACATTAAGCCTGAGAGAA

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FIGURE 186

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKGNGYVQSPRF
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETSTIIRGRWCG
HKEVPPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDQPAAASETNWESVTSSISGVSY
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSG
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 270-274

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 262-266

Tyrosine kinase phosphorylation site.

amino acids 256-265

N-myristoylation sites.

amino acids 94-100, 186-192, 297-303, 298-304

TonB-dependent receptor proteins signature 1.

amino acids 1-56

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FIGURE 187

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCTGGGGACGGCAGTCCCTG
TGTCTCTGGTGGTTGCCTAACACCTGCAAACATCACCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
CATATATGGGAAAAGAAATGGCTGAATAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTCTGCTGAAACTCTGACTACGAACACCAGTATTATGCCAAGTTAAGGCCATTG
GGGAACAAAGTGTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGTCCTGACAGCTCC
AGAGAAGTGBAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTTGAATACTAAACAGAACGTGGTCCCAGTGTGACCAA
CCACACGCTGGTGTCACCTGGCTGGAGCCGAACACTCTTACTGCGTACACGTGGAGTCCTT
CGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTGCCAGGACTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTGCCATATCTATTACCGT
GTTCTTTCTGTGATGGCTATTCCATCTACCGATATATCCACGTGGCAAAGAGAAACA
CCCAGCAAATTGATTTGATTTGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGA
AAAAATCGTGATTAACTTATCACCCCTCAATATCTGGATGATTCTAAAATTCTCATCAGGA
TATGAGTTACTGGAAAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCTCAGGAGGAAGAGGAGGTGAAACATTAGGGTATGCTTCGATTTGATGGA
AATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCACCCAGCAAGAGTCCCTCAG
CAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGGAGGAGGTGTCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCGAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGCCGGAGGA
AGAGCCATCGACGACCCCTGGTCAGTGGATCCCCAAACTGGCAGGCTGTGATTCCCTCGCT
GTCCAGCTCGACCAGGATTCAAGAGGGCTGCGAGCCTCTGAGGGGGATGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCAATGGAGGAATGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA
CTTCCCTTTGCCTTGTGCAAACAAAGTGTGAGTCACCCCTTGATCCAGCCATAAA
GTACCTGGATGAAAGAAGTTTCCAGTTGTCAAGTGTCTGTGAGAA

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FIGURE 188

MPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLKDDQSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHPANLILIGNEFDKRFFVPAEKIVINFITLNISDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHTMLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPPDKTVIEYEYDVRTTDICAGPEEQELSLOEEVSTQGTILLESQAALAVLGPQLQYSYTP
QLQDLDPLAQEHTDSEEGPPEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGGLGEE
GLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMAN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

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FIGURE 189

ATGTGCTGGCCGCTGCTCCTGCTGTGGGGCTGCTCCCCGGACGGCGGCCGGGCTCG
GGCGAACCTATCCGCACCGGACCCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC
CAGCGGGGCAGCCAGATCGCCTCCGCCTCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC
TTCTCGCCCACCGGGGCCATGGCGTCCGCGACATCGTGTGGCGGGGTGGCCACGGCGG
CCCTACCTCCAGGATTATTTACAATGCAAATAGAGAGTTGAAAAAAGATGCTCAGCAAGAT
TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTACAGAGAGCTG
CATACATGTGACATAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCTAC
CACCATGAAGATGCAGGAGAAGCTGGTCCAAGTACCATGACTCCAATAGGGGCACCAAGAGT
TTGCGGTTATTGAATCCTGAGAAAATAGTGTGCTATCTACAGCCTTACCATACCTTGATCTG
GTAAATCAGGACGTCCCCATCCCAAACAAAGATACACATATTGGTGCCAAATGTTAAGATT
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG
AGTCTGGTGACACCACATCCTGCTCTACAGTCAGCAACAACCTTAACGACAGCGTTCTGGAG
TCCGGCCACGAGTGCTATCACCCAAACATGCCGATGCATTCTCACCTGTGAAACTGTGATT
TTTGCCTGGCTATTGGTGGAGAGGGCTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACCTATGAGGAA
GGCTTAATAGATAATTCTGGACTGAGGTTATTTACACAATGGATATAAGGAAATATGATGCT
GGGGTGGATTGAGGCTGGCCTCTGGGTGAGCCTTCCATACCATCCCTCAGGGATGCCTGAG
TTCCAGTCTGAGGGTCACTGCACTTGGAGTGCCCTGGAAGAGGGCTCTGGAAGCCGAAAAGCCA
AGTGAATTCATGTGTTGCTGTTCTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG
CGTCATTTGAAAAGGGAAGGAAATGAAATTACTTGCTATGATGATGATTTGACTTCAT
TTCCAGGAGTTCACTAAAGGAAGAACAAACATCTTACAGGAGATAACCTAATTACT
GAGTGTGCTACAACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAACGACCAAGGAGT
GAAATGTGCTCTCATACCTCTTATTACCCAAGAATTAAATCTTACTCGATGTGCAAGTATT
CCAGACATTGGAACAACCTCAGTTCATGGGTTAAGGAGATCTACAGACCAGTCACGACC
TGGCCTTCATTATCAAAGCTTCAAGCAATATAAAACCTTCTTCATGGATGCTATGAAT
AAGTTAAATGGACTAAAAGGAAGGTCTCTCCTCAACAAGCTGGTCTCAGCCTGCCAGTG
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGCTGATTCAAGGAATGACAGCATTACCT
CCAGATATAGAAAGACCCCTATAAACGAGAACCTTGGTGTGTCAGCTGACGCTGAGC
CTGCACAGAGATTCTCCATCAACTTGCTGTTGCCCTCTGCTACTCAGCTGACGCTGAGC
ACCAAGAGCTTG**TGA**TCAAATTCTGTTGGACTTGACAATGTTCTATGATCTGAACCTGTC
ATTTGAAGTACAGGTTAAAGACTGTGTCACCTTGGCATGAAGAGTGAGGACTTTCTTC
CCCATTTCCTCCCTCTTCTCATGTTACATGAGAGACATCAATCAGGTTCTCT
CTCTTCTTAGAAATACCTGATGTTATATACATGGTCAATAAAATAAAATGGCCTGACTT
AAGATAACCATTAAAAATTGGGCTGTCATGTGGAATAAAAGAATTCTTCTTCCTAA
AAAAAAA

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FIGURE 190

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLLDSEGYWLGSQRGSQIAFRLQVRTAGYVGFG
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIIEFTREL
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGKSLRLLNPEKTSVLSTALPYFDL
VNQDVPIPINKDTTYWCQMFKIPVFQEKKHVKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE
SGHECYHPNMPDAFLTCTEVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEE
GLIDNSGLRLFYTMIDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCLECLEEALEAEKP
SGIHFVFAVLLHAHLAGRGIRLRHFRKGKEMKLLAYDDDFDFNFQEFOYLKEEQTILPGDNLIT
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT
WPFIKIHKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLSPVNVRCSKTDNAEWSIQGMTALP
PDIERPYKAEPPLVCGTSSSSLHRDFSINLLVCLLLSCTLSTKSL

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 56-73, 378-393, 583-602

N-glycosylation sites.

amino acids 114-118, 247-251, 476-480, 517-521

N-myristoylation sites.amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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FIGURE 191

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTCTGCTTCTGTTCTTATAACAT
TTTCTTCTGCATTCCCTTAGTCGGATGACGGAAAATGAAGAAAATGCAACTGGCTCAGG
CATATCTCAACCAGTTACTCTCTGAAATAGAAGGGAATCATCTTGTCAAAGCAAGAATA
GGAGTCTCATAGATGACAAAATTCGGAAATGCAAGCATTGGATTGACAGTGACTGGAA
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCCTGATGTGGCC
AGTATGGCTACACCCTCCCTGGTGGAGAAAATACAACCTCACCTACAGAATAATAACTATA
CTCCGGATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTAGAAGTGTGGAGCA
AAGTCACTCCACTAAAATTACCAAGATTCAAAGGGGATTGCAGACATCATGATTGCCTTA
GGACTCGAGTCCATGGTCGGTGTCCCGTCTGCTATTGATGGTCCCTGGGAGTGCTTGGCCATG
CCTTCCTCCTGGTCCGGGCTGGTGGTGCACACTCATTTGATGAGGATGAAAATGGACCA
AGGATGGAGCAGGATTCAACTTGTCTGGCTGCTCATGAATTGGTCTGACTGGGC
TCTCTCACTCCAATGATCAAACAGCCTGATGTTCCAAATTATGTCTCCCTGGATCCCAGAA
AATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG
TACCTGCTAACGCAAAGGAACCCACTATAACCCATGCCTGTGACCCGTACTGACTTTGACG
CTATCACAACTTCCGCAGAGAAGTAATGTTCTTAAAGGCAGGCACCTATGGAGGATCTATT
ATGATATCACGGATGTTGAGTTGAATTAATTGCTTCATTCTGGCCATCTGCCAGCTGATC
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTGTTAAAGATGAAAATCTCTGGA
TGATCAGAGGATATGCTGTCTGCCAGATTATCCCAAATCCATCCACATTAGGTTTCCAG
GACGTGTGAAGAAAATAGATGCAGCCGTCGTGATAAGACCACAAGAAAAACCTACTTCTTG
TGGGCATTGGTCTGGAGGTTGATGAAATGACCCAAACCATGGACAAAGGATCCCGCAGA
GAGTGGTAAACACTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGAT
TCTTCTTTTCAGCCGTGGATCAAAGCAATTGAATACAACATTAAGACAAAGAATATTACCC
GAATCATGAGAACTAATACTGGTTCAATGCAAAGAACCAAAGAACCTCCTCATTTGGTTTG
ATATCAACAAGGAAAAGCACATTCAAGGAGGCATAAAGATATTGTATCATAAGAGTTAAGCT
TGTTTATTTGGTATTGTTCAATTGCTGAAAAACACTTCTATTATCAATTAAATTCAAGAC
CTAAAATAAACCTAACAGGTCTTTAATATAAATTCTGCTCAAAATAGAATAAAACCATTG
TTAACAAAC

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FIGURE 192

MKRLLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEGNHLVQSKNRSLIDDKI
REMQAFFGLTVTGKLDNSNTLEIMKTPRCGVPDVQYGYTLPGWRKYNLTYRIINYTPDMARAA
VDEAIQEGLLEVWSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFFFFPGL
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMFVNYSLDPRKYPLSQDD
INGIQSIYGGLPKVPAPKKEPTIPHACDPDLFDAITTFRREVMFFKGRHLWRIYYDITDVEF
ELIASFWPSLPADLQAAYENPRDKILVFKDENCWMIIRGYAVLPDYPKSIHTLGFPGRVKKIDA
AVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFPQRVVKHFGISIRVDAAFQYKGFFFFSRGS
KQFEYNIKTKNITRIMRTNTWFQCPEKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH
LLKNTSIYQ

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

N-myristoylation site.

amino acids 71-77, 205-211, 223-229

Hemopexin domain signature.

amino acids 171-202, 207-238, 318-334

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 213-223

Matrixins cysteine switch.

amino acids 89-97, 207-238

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FIGURE 193

CACAATCAGGTCCCATTCTATAGATGGGAAACTGAGGCTTGAGGTACATAGGCCTCGTTCA
AGGCTGGTATAACCTGCACCCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGCTGTCA
TCCAGTCTCCTCCCTGCCCTGCTGGTGCACTTCCCTGCCTCTGCTGGTGCACTTCTGCCCT
ACTGGTATATTGCTGCCTCTGCTGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCT
GCTGGTGCACTTCTGCCCTGCTGGTGCACTTCCCTGGCTTGCTGGCGACTTCCCTGCCCT
GCTGGCACACTCCTGCCTCTGCTGGTGCACTTCCCTGGCTTGCTGGCGACTTCCCTGCCCT
TGCTGGTGTATTCCTGCCCTGCTGGTGTACTTCCTCCCTGCTGGTGCACTTCCCTGCCCT
TGCTGGCGACTTCTGCCTCTCCAGGCCCTACCTAGCCTCTCCCTTTATATGGAAGTCT
TCCCAGTTCACTGACACTGGTAACAGGGACTCTGCTCTGGTGTGCTGCCCTGGGAT
GGGCATCTGTGTCTTCCTTACTACTGCTGGCTCAGGACCCAGAGCTTGAAGCATGTCCAGA
TGCAGGTCCGGGACCAAGAGTCTAAGGAGCCCTACACCCACCAGGATTTCCAATAAGAGA
TGTTCACCA

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FIGURE 194

MVLGNGGCHPVSSLPLLVHFLPLLVLVYLLPLLGRFLPRLVYLLPLLVLHFLPPLMHFL
PLLVLHFLALLAHFLPLLVLHFLALLAHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

Signal peptide:

amino acids 1-39

N-myristoylation sites.

amino acids 4-10, 109-115, 116-122

Leucine zipper pattern.

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,
65-87, 66-88

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FIGURE 195

GGCAAGGCGCGGCGGCAGCCGGTGGCGGTGGGAACATCTCGGCAGCCA
CCGCGCTTCTCCCGCTGGAGCGGGCGTCAGCTGGCTGCCCTCGGTCTCCCTGCCACGTT
TCGGGTGCCCTGCACCCCCCACCAGGCTCGCTCTTCGAAGCGGGAAAGGGCGCTTGCA
GGATCCTGCCGCCCTCCAACCGGATCCTGGGTCTAGAGCTCCCAGAGCGAGGCCTGCCA
GGACTCCTGCCGCCAACCCCTGACCGCCGGGGGTGCCCTGGGACGTAGCGCCGCGGAGAG
GAAGCGGAAAGGGGACC**AT**GCAGCTGACTCGTGGCTGGTCTGCCAGTCTCGGGTG
CTCTGGATCACGGTGCTGTTCTGGTAACAAGAGGAAGTTGGAGGTGCCGACGGGA
CCTGAAGTGAGACCCCTAACGCCTCGGACGCTGACTGGGACGACCTGTGGGACCAAGTTGAT
GAGCGGCGGTATCTGAATGCCAAAAGTGGCGCGTGGTGACGACCCCTATAAGCTGTATGCT
TTCAACCAGCGGGAGAGTGAGCGGATCTCCAGCAATCGGGCATCCGGACACTGCCATCTG
AGATGCACACTGCTGGTGATTGCACGGACCTCCACCCACTAGCATCATCATCACCTTCCAC
AACGAGGCCGCTCCACGCTGCTCAGGACCATCCGAGCTGATTAAACCGCACCCCTACGCAT
CTGATCCGGAAATCATATTAGTGGATGACTTCAGCAATGACCCCTGATGACTGAAACAGCTC
ATCAAGTTGCCAACGGTGAATGCTTGCAGAATAATGAACGCAAGGTCTGGTCCGGTCCCGG
ATTGGGGCGCTGACATGCCAACGGCACCCTGACTTTCTCGACAGCCACTGTGAGGTG
AACAGGGACTGGCTCCAGCCTCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGTG
CCTGTATCGATATCATTAACCTGGACACCTCACATCGAGTCTGCCCTGGAGCTCAGA
GGGGGTTTGACTGGAGCCTCACTCCAGTGGAGCAGCTCTCCCAGAGCAGAAGGCTGG
CGCCTGGACCCCACGGAGCCATCAGGACTCCTATCATAGCTGGAGGGCTTCTGTGATCGAC
AAAGCTTGGTTGATTACCTGGGAAATATGATATGGACATGGACATCTGGGGTGGGAGAAC
TTTGGAAATCTCTTCCAGTGTGGATGTGGGGCAGCCTAGAGATCGTCCCTGAGCGA
GTGGGGCACGTCTCCGGAAAGAACGACAGCTAACGCTAGTGTGGATGGATGAATACAAGCA
ATAAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAACTATTACGCT
GCCGGCCATTGCCCTGGAGAGGCCCTCGGGAAATGTTGAGAGCAGATTGGACCTGAGGAAG
AATCTCGCTGCCAGAGCTCAAGTGGTACCTGGAGAATATCTACCCCTGAACACTCAGCATCCCC
AAGGAGTCCTCCATCCAGAACGGCAATATCCGACAGAGACAGAACGCTGGAAATCTCAAAGG
CAGAACACCAAGAACCCCAAACCTAAAGTTGAGCCCTGTGCCAAGGTCAAAGGCAGAGAT
GCAAAGTCCCAGGTATGGCCTTCACATACACCCAGCAGATCCTCCAGGAGGAGCTGTGCTG
TCAGTCATCACCTTGTCCCTGGCGCCCTGGTCTTGTCTTGTCAAGAATGGAGATGAC
CGACAGCAATGGACCAAAACTGGTCCCACATCGAGCACATAGCATCCACCTCTGCCCTGAT
ACAGATATGTTCGGTGATGGCACCGAGAACGGCAAGGAAATCGTGTCAACCCATGTGAGTCC
TCACTCATGAGCCAGCAGCTGGGACATGGTGAGCTCT**TGA**GGACCCCTGCCAGAACGAGCAAGG
GCCATGGGGTGGTCTCCCTGGACCAAGAACAGACTGGAAACTGGGAGCAGCAAGCAGCCTGCCA
CCACCTCAGACATCCTGGACTGGGAGGTGGAGGCAGAGCCCCCAGGAGCAGGAGCAACTGTCT
CAGGGAGGACAGAGGAAACATCACAGCCAATGGCTCAAAGACAAATCCCACATGTTCTCA
AGGCCGTTAAGTCCAGTCCTGGCCAGTCATTCCCTGATTGGTATCTGGAGACAGAAACCTAA
TGGGAAGTGTATTGTTCTTCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAAG
CCTTCTTTCACTAGGCCAGGACTACATTGAGAGATGAAGAATGGAGGTGTTCCAAAAGA
AATAAAGAGAAACTAGAAGTTGTCTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA
AAAAAAGAAAAAAGAAAAAAG

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FIGURE 196

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPPTSIIITFHNEARST
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPVKCLRNNERQGLVRSRIRGADI
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVPIDIINLDTFTYIESASELRGGFDWS
LHFQWEQLSPEQKARRLDPTEPIRTPIIAGGLFVIDKAWF DYLGYDMDMDIWGGGENFEISFR
VWMCGGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYAARPFFAL
ERPGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQET
PNLKLSPCA KVKGEDAQSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK
TGSHIEHIASHLCLDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

Transmembrane domain:

amino acids 475-493

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 2-6

Tyrosine kinase phosphorylation sites.

amino acids 68-75, 401-409

N-myristoylation sites.

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

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FIGURE 197

GCAGCTCACCCCTCGCAGCCCG**GATGGGG**AAGACGACGCCGCCTCGGGCTGGCAGCAGGGGCTCTCCGACC
 CGTGGCAGACTCAGTGGGAGTGCACCCGCACCACGGAGGCCACATCGCCGTACACAAGCGGCTTGTGCTGG
 CCTTCGCTGTGTCCTCGCATTGCTCGCGGTACAATGCTCGCTGTGCTCAGCCTCGCAGCAGT
 GCGGGCGAGTGCCACGCCAGGCGCCACGGTGGCCCTCAGGCTTCCGGAGGCCGGCAACGGGAGCC
 CTGGATCGGCCCGGCCAACACCACGCCAGGGGGACTCCTGGCAGCCCAGGGGGAGCCGTGGACGCAGCTGCC
 GGACCAACGTGCCCGCAGGCCGTGGAGGAGGCCGGAGCCGTGGACGCAGCTGCCCTGTGG
 GCCACACTGAAGCCGCTGCACTACAATCTGATGCTCACCGCCTCATGGAGAACTTCACCTTCTCCGGGAGGTCA
 ACGTGGAGATCGCGTGCCGGAACGCCACCCGCTACCTAGTCTGCACGCTCCGAGTGGCGTGGAGAAAGTGC
 AGCTGGCGAGGACCGGGCGTCCGGGCTGTCCCTGTAGCGTTTCTCTACCCGAAACCCAGGTCTTAG
 TGGTGGTGTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACACGCCCTCATCGAGA
 ATGAGCTCCTGGCTTCTCCGAGCTCTATGTGCTCACGGGGAGAGAAGAGATTCTGGTGTACTCAGTTT
 CGCCTACACATGCCAGAAAGCATTCTGTGTTGATGAGCCAATCTACAAGGCTACTTCAAATCAGCATCA
 AGCATCAAGCAACCTATTTATCTAATATGCCAGTGGAAACTTCCGTGTTGAGGAAGATGGATGGGTTA
 CGGATCACTTTACAGACCCCTCTCATGTCCACATATTATTAGCCTGGCAATTGCAACTCACATACAGAG
 AAACCTACCAAGACTGGGGTTGTAGTACGATTATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGACT
 ATGCTCTCCATATAACAAAGAGATTAATAGAATTGAGACTACTTAAAGTGCCTATTCTTGCCAAA
 TAGATCTTAGCTGTGCCCTAACGCATCCGTATGCTGATGGAGAACTGGGGACTAAGTATTTGTGGAACAAA
 GAATACTGCTGGATCCCAGTGTTCATCTATTCTATTGCTGGATGTCACCATGGTCATTGTCATGAGATAT
 GTCACCAAGTGGTTGGTACAGACTACCTCTATCTGGCTGGAACATGGAAACAGCAGAGGTTCTGACCGATGTT
 TGCAATGAGTGTGCTGACGGTTGGCCAGTCCCATCAGTATCACAGGAAGTGTGCTGCAGGCAACAGATA
 TTGACAGGGTGTGTTGACTGGATCGCATATAAAAGGGTGTGCTTAAATAAGAATGCTGGCTAATTG
 ATTCACTGTTCCAGGGGTTGCAAGATTATAACCATGTAATGTAATATAAGAAGTGGATCAGTGGACAC
 GGAATACATTATCAGGGCTTAAAAAGAAATGGAAATATGTAATATAAGAAGTGGATCAGTGGACAC
 TCCAGATGGGTTCTCTTATCACCATCTGGAAACACAAACAGCAGAAATAGAATAATAATTACCAACAGC
 ATTTTATCTATGATATCAGTCTAAAACAAAGCACTTAAACTCAGAATAACAGTACCTGTGCAAGATTCC
 TAACATTGTGGTAGGAAATAGAAGCCATGTGCTCAGAAGCAATTATTGGGTGCTAACAAATCAGAGCACC
 ACAGAATAACTTATTGACAAAGGAAGCTGGCTGGGGACATCAATCAAACAGTGGCTATTAGAGTCAACT
 ATGACCTAAGGAACGGAGATTATTAATTGATCAATTAATCCGAATCATGAGGTTCTCTGTCAAGTAACCGAG
 CGGGCTTGATCGATGATGCCCTCAGCCTAGCCAGGGCTGGCTATTGCTCAGAATACTCTGGAGATTATCA
 GATACCTGCTGAGGAGAAGGATTCTCCTGGCATGCTGCCAGCCAGCTTTATCTCTAGATAAATTAC
 TGGACCGCATGGAAACACTACAACATTCAATGAATATTTAAAGCAAGTGTCAACAAACATATCAAGCTTG
 GGTGGCCGAAAAATAATTAAATGGATCTTGTCAAGCATCCTACCAACATGAAGAACTACGTAGAGAAGTTA
 TAATGCTGGCTGCAGTTGGCAACAAGCACTGTCACCAACAGGCATCAACACTTATTCAGATTGGATTCCA
 GCAACAGGAACAGAATACCAACTAAATGTTAGAGACATCGTACTGTACAGGAGTGTCACTACTGGATGAGGATG
 TCTGGGAATTCATATGGATGAAATTCCATTCCACACAGCAGTTCTGAGAAGAAAATATTATGGGAAGCCTAA
 CTTGCACTGATGACAGGAATTATTAACACAGGCTCTAAATCTGCACTGAAATTCTGGAGGTGGTGTGATCAAG
 ATGCAATTGATGTCATAATCATGTCAGCTGCAAAATCCACATGGTCAGACCTTGGCTGGAGTTTCAAGGATA
 AATGGGAAGATATTAAATACCAAGGTATGGAGAAGCATTGTTATGTTTATCTTCAACTCATCAGTGGTGTACAGAAT
 TTCTTAATACTGAAGGTGAACCTAAAGAGCTCAAGAACCTCATGAAAACATGATGGGGTAGCTGCTGTTCT
 TCTCACGAGCTGGAAACACTGCAAGCCAATGTGCGCTGGAAAATGCTTACCAAGACGAGCTTCAATGGT
 TAGGAAAAGCTTAAGACACTAAATATGTTATCTTAAACAAACATTCAACTCAGAAGTTATGAGAAGACAC
 GCTTTTGGAATGAGGAAATGTAACCTAGAAAATGCCAGATTTCAGTGTAACTGTTGAGGAGAATT
 TTTTTTTAGTTTATTTGGTTGGGGATATTCTTATTGTTCTCATCATTCTGTTCTGTTCT
 TGGGTGTTCTCTAAAGAAACCTTGTCAAGTGAACACTAGCCATGATTGCTTCAGCTGTACATTCTTGCTGTA
 CAGGACCAAATATGATAGTGTGATGCATGTTGATGTTACAGTCATTGAGGAAACATATTCAAGAATATCTGTGCA
 GGATATATTGTCCTGCCTGTTCCAGCATGCTTAAACGTCAGTGTGTTGAGAATATGTGTTACACC
 TAGGATGGGCATTATGCAAAAGCACAAAGATTATATGACAATCAGTATTGCAATGAAAGAAAACACTAAA
 GAAATGATATTCTCAATTGGCAATGTGAGAGGAAAATAGCCCTGACATGATGAACATCACTTATTCT
 ACTTGGATTGTCGGCAATGATTACTGTGTTGCTAACATCATTCTTGAGTTAAAGCTGTGATACATTAA
 AGGCATATAGATAGTGTATGCATATGTATATGTACATAGGGAGCCCATATGTATATAGTATGTGTCACACTGC
 ACATGTACAAAGAATGTCTCAGATCAAAGAAAATTATCTCTTTATAAACTTAAGGACAGTTGCAAAAGGCT
 TCAAGGAATTATCTCAACATTATTCTTCTATGTCTAACCAAATTCTCAACTGTTATGAAATTCTCATCTAC
 TTCTTGAAACAGTGGTCTATTCTGCTACATGAAGATGAATACAAACAAATTGGTATAAACTCCCCAAAAAAA
 AAAAAAAA

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FIGURE 198

MGEDDAALRAGSRGLSDPWADSGVVRPTTERHIAVKRLVLAFAVSLVALLAVTMLAVLLSL
RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHHAGGDSWQPEAGGVASPGTTSAQPPS
EEEREWPWTQLRLSGHLKPLHYNLMFTA FMENFTSGEVNVEIACRNATRYVVLHASRVA
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLGFFRSS
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG
WVTDHFSQTPLMSTYYLAWAICNFTYRETTKSGVVVRLYARPDAIRRGSGDYALHITKRLIE
FYEDYFKVPYSLPKLDLLAVPKHPYAA MENWGLSIFVEQRILLPSVSSISYLLDVTMVIVHE
ICHQWFGDLVTPVWWEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDLHEVMLLDGLAS
SHPVSQEVLQATDIDRVFDWIAYKKGAALIRMLANFMGHSV FQRGLQDYLTIHKYGNAARNDL
WNTLSEALKRNGKYVNQEVMDQWTLQMGPVITILGNTTAENRIIIITQQHFIYDISAKTKAL
KLQNNSYLWQIPLTIVVGNRSHVSSEAIIWVSNKSEHHRITYLDKG SWLLGNINQTGYFRVNY
DLRNWRLLIDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLEIIRYLSEEKDFLPWHA
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNFNGSLVQASYQHEELRREVIM
LACSFGNKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSSLDEDVWEFIWMKFHSTAV
SEKKILLEALTCSDDRNLNRLLNLSLNSEVVLQDAIDVIIHVARNPHGRDLAWKFFRDWK
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAASFSRAVETVEANVRWKM
LYQDELFWLGKALRH

Transmembrane domain:

amino acids 44-63

N-glycosylation sites.

amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,
634-638, 649-653, 663-667, 684-688, 800-804, 906-910

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 362-366

Tyrosine kinase phosphorylation site.

amino acids 520-528

N-myristoylation sites.

amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,
825-831, 987-993

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 437-447

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FIGURE 199

GGCAGCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGTCCGCCAGGGGCTCCGAAGCTGCC
GGCCCGGGGCTCCTCCCTCGCTCCGCTCCCCCTCGCTCACGCCGCCCTCCTCCCCAGCTCCCTCGCC
GTCCGGCCGCCCCACAGCCAGCGGCTCCGCCCTGCAGCCACGATG
ACTCCGGGGATCTCGTGTCTCGCTCTGCTCTGGGAGCCGGCAGCGAGGAGATGCTCTTC
CGAGGGAGATGCTAGCCCTTGGGCTCTAACCTCTGCCCTCAGGAGCCCCGGAGAGAGGCAGTCCTGGCAAAGA
GCACCCCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCTCACAGT CGGCGGAAGTGTCTGGCGAGCTGGTGT
GGATGGGACCGCACCTCTGCACATCACGACATCCCAGCCCTGTACCCTGCTCTCCAGAGGAGGCCGCC
GCACGCCCTGCCCTCAAGAAGAAACTGCCTCTGCCTCAAGCAGGTGA
GCCACCTCCGAGCCACTGTCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCTAGATCTCTCTCT
CACGGAGAAGGCTGCCAACGGGGGACCGGACCCCATCGTGGCTCCGAGGAGGCATCAGAAGTGCCCTT
GCTGGATCGAAAGGAGAGTGGGCTCCCTACAACACCCGACCCCTGCAAATCTCCCCCTCACTTCGAGGCC
TGTGGCCACACACTCCCCAGAGGCCAGAACCGGGAGCTGGGCTGACATGGCCAGGGCAGGCC
GGACACCCAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTCAGCCTCAGAGGAGGCC
GACCACTACCTCCACCATATTACCAACACGGTCATCACCACCGAGCACAGCACCAGCTCTGCAGTGTGAGCT
CTCCAATCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAACTTCTGGAGTGACATA
CAACGTGACAGTCAACTGGATGGGCTCCAGGTGAAGAGTGTGAAACCTGTCCGATGGGAACTGCT
CTCCATCCGGGGGCTGGACGGGCTTACCCCTGACCGTCTGGCCAACCCAGACACTCCTGGTGGAGGGCAGGTAA
CCGAAGGCCACCAACACCATCTCGTCACTTCCGACCTCCAGGACGACGGCCTGGGACCTCCAGCTCA
CTACCAAGGGCTTCATGCTGAGGTGCAACTTCCCCGGCCTGACTCTGGGATGTACGGTGATGGACCTGCA
CTCAGGTGGGTGGCCACTTCACTGCCACCTGGCTATGAGCTCAGGGCTAAGATGCTGACATGCA
TGCCTCAAAGCGCACTGGAGCAGCCAGGAGCCATCTGTCAGCTCCTTGTGGAGGGGCACTGCA
CATGGCCGCTCTCCCCAAGTTACCTGAAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAGC
TCCAGAGGGCCAGAAGCTGACCTGCACTTGAGAGGCTGTTGTCATGACAAGGACAGGATGACGGTT
CGGGCAGACCAACAAGTCAGCTTCTCTACGACTCCCTCAACCGAGAGGTGCCCCTTGAGGGCCTGCTGAG
CGAAGGCAACACCATCCGATCGAGTTACGTCGACCAGGCCGGGGCCTCCACCTCAACATCCGATTGAG
AGCCTTGGAGAAAGCCACTGCTATGACCTACATCCAGAACTTCACTACATCCGACCCGACCTATA
CATGGGACTATAGGGAGTTACCTGCGACCCGGCACTCCCTGGAGCAGGGCCGATCATCGAATGCA
CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGAGGCCATGTGTTGGGGAGCTCTGCTG
GGCTGGGTGGTATTGCCCCAACTGCCCGAGCCCTACGTGGAGGTGAAGATTGTATCTGGAA
GGGAGAAGAGAAACGGATCTCTTAGATACTCAGTTCTGAGCAACAGTGCACATCTGACCATCTAC
TGGCGACGAGGTCTGGCCACATCTGGGAGCTACCTGGGAAACAGTGGGCCCCCAGAAACTGTA
GCCAGACTTAACCATCCAGTTCATTGGACCCCTGCTGGCCTCATCTTGGAAAGGGCAGGGATTATCATG
CTACATAGAGGTATCAAGGAATGACTCTGCTCGGATTACCCAGATGGCTGGAA
CACGGAGTTGGTGGGGGAGCAGAACATCACCACCGTGTGACCCGGCTATGACATCTGGGAGTGAC
CACCTGCCAGTGGGACCTCAGCTGGAGCAGCAGGCCCTATTTGTGAGAAAATTATGTA
AGAGGTGGATCACTCGACCCGCTTAATTCCGATCTGTGCTGTTGGGACCCATCCA
CCCCGGTTTGTGCTGGAGGGAGTTCTCTGGACCTGCTACAGCCGTGAAACAGGGACTCC
TCGGCTGGCCCACTGGCTTCCGGAGGAGTCCCTGGCATGTGACAA
CTCTGACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTCATGTGCTACGAAGGCTTGT
AGTGCACCATCCGCTGCATCTGGACAGC
CAGTTTGAAACATGCTTGTAGAGCAGAACGGCAGCAGAGACGTC
CTTCACTCCGGTCTCATCATCTCTTACTGCTGGGAGGAGCCTACATT
CAACCTCCGCTGCTGATGACTCCACCCCTACAGCCAGATCACCGTGGAA
TTACGAGACAGGGGAAACCGAGAGTGTAGGTTCTATCTAA
CTCAACACAAATCTCTCGAGACATTCATCCAGAGACCATGTGGCA
CTTTGTTAGACTCTTATCAAAGTTACTGTTCTCCCTGTATTTATT
AAAAAAAAAA

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FIGURE 200

MPAARPPAAGLRGISLFLALLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE
ERVVTAPPSSSQSAEVLGELVLDGTAPSAAHDIPALSPLLPEEARPKHALPPKKLPSLKQVN
SARKQLRPKATSAATQRAGSQPASQGLDLLSSSTEKGPGPPGDPDPIVASEEASEVPLWLDRK
ESAVPTTPAPIQISPFTSQPYVAHTLPQRPEPGPDMQEAPQEDTSPMALMDKGENELTG
SASEESQETTSTIITTVITTEQAPALCSVFSNPEGYIDSSDYPLLPLNNFLECTYNVTVY
TGYGVELQVKSVNLSDGELLSIRGVDGPTLTVLANQTLVEGQVIRSPNTISVYFRTFQDDG
LGTFLHYQAFMLSCNPRRPDSGDVTVMVLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW
SSQEPICSAPCGGAVHNATIGRVLSPYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEKGHC
YEPMIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPAAIECINVRDPYWNDTEPLCRAMCGG
ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEVMPHI
LGQYLGNSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK
TTSHTELVRGARITYQCDPGYDIVGSDTLCQWDLSWSSDPPFCEKIMYCTDPGEVDHSTRLI
SDPVLLVGTTIQYTCNPFGVLEGSSLTCYSRETGTPIWTSRLPHCVSEESLACDNGLPENG
YQILYKRLYLPGESLTFCMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA
AAETSLEGGNMALAIFIPVLIISLLLGGAYIYITRCRYYSNRLPLMYSHPYSQITVETEFDN
PIYETGETREYEVSI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 893-915

N-glycosylation sites.amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

N-myristoylation sites.amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

FIGURE 201

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGCTCCTCGCCTTCT
GTCTTCTGCGTCTACTAGCAGGTTGTGCAGGGAAACTCAGTGGAGAGGAAGATATATAT
CCCCCTAAATAAAACAGCTCCCTGTGTCGCCTGCTCAACGCCACTCATCAGATTGGCTGCCA
GTCTCAATTAGTGGAGACACAGGGTTATCCACGTAGTAGAGAAAAGAGGGAGGACCTACAGTG
GGTATTGACTGATGGCCCCAACCCCCCTACATGGTCTGCTGGAGAGCAAGCATTTCACAG
GGATTAAATGGAGAAGCTGAAAGGGAGAACCCAGCGAATTGCTGGTCTGCAAGTGTCTTGAC
CAAGCCCAGTCCTGCCTCAGGCTCTCTCTAGTGTACAGTGCCAAATGATGGTTGGTGT
TTACTCCAATTCCATGGGCCAGAGTTGCTCACTGCAGAGAAAATACAGTGGAAATTGCTGGG
CAATGGTTGGCTTATGAAGACTTAGTTCCCCATCTTCTTCTGAAGATGAAAATGAAAC
CAAAGTCATCAAGCAGTGTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT
CCCACATGTGCCATGCAGCTTTACACATGCATGTCATCAGCACTGCCACCTGCAT
GCAGCGCAGCTCCATCCAAAGCACCTCAGCATCAACCCAGAAAATCGTCTGTGACCCCCCTGTC
TGATTACAATGTGTGGAGCATGCTAAAGCTATAAATACAACGGACATTAAAGCCTGACGA
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTCTTTCTGGAATGTGGCCCCAGG
GGCTGAAAGCGCAGTGGCTTCCTTGTCAACCCAGCTGGCTGCTGAAGCTTGCAAAAGGC
ACCTGATGTGACCACCCCTGCCCGCAATGTATGTTGTCTTTCAAGGGAAACTTTGA
CTACATTGGCAGCTCGAGGGATGGTCTACGATATGGAGAAGGGCAAGTTCCGTGCAGTTAGA
GAATGTTGACTCATTGAGCTGGGACAGGTGGCCTTAAGAACTCATTAGAGCTTGGAT
GCACACAGATCCTGTTCTCAGAAAAATGAGTCGTACGGAACCCAGGGTGGAGGATCTCCTGGC
CACATTGGAGAAGAGTGGTGCCTGCTGCTGCTGCTGATCCTCAGGAGGCCAAATCAGTCCA
GCCTCTCCCACCATCTTCCCTGCAGCGATTCTTCAGCTGAAACATCTGCGTTGTCT
GGCTGACCAACTCTGGTGCCTCCATAACAAATATTACAGAGTATTACGACACTGCTGAGAA
CATTAATGTGAGCTATCCGAATGGCTGAGCCCTGAAGAGGGACCTGAACACTTGTAAACAGACAC
TGCCAAGGCCCTGGCAGATGTGGCACGGTGCTGGACGTGCTGTATGAGCTGCAAGGAGG
AACCAACTTCAGCGACACAGTTCAAGGCTGATCCCCAAACGGTTACCCGCTGCTATGGGTT
CCTGATTAAAGCCAACAACATGGTCCAGTCATCCTCAGGCAAGGACCTAACGGCTACTT
GGGTGACGGGCCTTCAACATTACATCGCTGTCTCAGCCCCACCAACACCACCTATGTGT
ACAGTATGCCTTGGCAAATTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCAGGA
TCCAAGTAAAGCTCAAGTGAAAACAAGGATCTGTATGAGTACTCATGGTCCAGGGCCCTT
GCATTCTAATGAGACGGACCGACTCCCCGGTGTGCGTTACTGCACGATTAGCCAGGGC
CTTGTCTCCTGCCTTGAACTGAGTCAGTGGAGCTACTGAATACTCATGGACTGAGAG
CCGCTGGAAAGATATCCGTGCCCGATATTCTCATCGCCAGCAAAGAGCTGAGTTGATCAC
CCTGACAGTGGCTTCGGCATCCTCATCTCTCCCTCATCGTACCTACTGCATCAATGCCAA
AGCTGATGTCCTTTCTATTGCTCCCCGGAGCCAGGAGCTGTCATAACT**TGA**GGAGGACCCCA
GCTTTCTGCCAGNTCAGCAGTTCACTTCTAGAGCATCTGCCCAGTGGGACACAACCAACT
AATTGTCAGTGGAACCTCCCTGGCCTGCTCAGATTGGGATTAACATAAAAGAGTGGAACT
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCTCCCTCCGCTCCCTTCCATCA
CCCCCTCCCCATTCCCTCTCTACTCATGCCAGATTGGGATTACAAATAGAAGCT
TCTTGCTCCTGTTAACTCCCTAGTTACCCACCTAATTGCCCTCAGGACCCCTACTT
TTCCCTCCTGCCCTGTACCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCT
GAAGTGGAAAGGACATAAAAGGTTAATGTCAGGGTCAAACACTACATTGAGCCCTGAGGACAGG
GGCAGCTCTGGCTGAGCCTACTGTCTCCTCCACTGTCCTTCTCCAGGCCCTCAGATGGC
ACATTAGGGTGGCGTGTGCGGGTGGGTATCCCACCTCAGCCCACAGTGTCAAGTGTACT
TTTATTAAGCTGTAATATCTATTGTTGTCTTTCTTTATTCTTTGTAAATAT
ATATATAATGAGTTCACTAAAGATTATCCC

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FIGURE 202

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNVERKIVIPLNKTAPCVRLLNATHQIGCQ
SSISGDTGVIHVVEKEEDLQWVLTDGPNPYMLLESKHFRDLMEKLKGRTSRIAGLAVSLT
KPSPASGFSPSPVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYERDFSPIFLLEDENET
KVIKQCYQDHNLSQLNGSAPTFPLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS
DYNVWSMLKPINTTGTLPDDRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAELQKA
PDVTTLPRNVMVFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVL
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLFNFVTDTAKALADVATVLGRALYELAGG
TNFSDTVQADPQTVTRLLYGF LIKANN SWF QSI LRQDL RSY ILGDGPLQHYIAVSSPTNTTYVV
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA
LSPAFELS QWS SSTEY STW TES RWK DIRARI FLIAS KELE LIT LT VFG I LIF SLI VT YCINA K
ADVLFIAPREPGAVSY

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 671-692

N-glycosylation sites.amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,
573-577, 580-584, 612-616**Glycosaminoglycan attachment site.**

amino acids 404-408

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 232-236

N-myristoylation site.amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

FIGURE 203

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCCTGCCAGGGAGCCGGGTTT
GAGCTCAGGCCTCTAGCGCCGGCCCCAGAAATCTGACTCGCAGGCCAGAGTTGCAGGG
CTGAATAGCAAACGTGAGGCTGAGTAGGAAACAGACCATGAGGTCAGTCAGATCTCCTCTCC
CAATGCCGTTGCTCCTCTACTAGTCCGACAATGCTCCTTAAGTCTCTGGCGAAGATGTA
ATTTTCACCCCTGAAGGGGAGTTGACTCGTATGAAGTCACCATTCTGAGAAGCTGAGCTTC
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCCTGTACCTACTGCAGTTAAAAGGCAAGAAG
CACGTCCCTCATTGTGGCCAAGAGACTCTGTTGCCCGACATCTGCCGTTTCTCCTTC
ACAGAACATGGGAACTGCTGGAGGATCATCCTACATACCAAAAGGACTGCAACTACATGGG
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGTCTCCGAGGT
GTATTTAACATTGATGCCAACATTACCAAATTGAGCCCTCAAGGCCTCTCCAGTTTGAA
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTGGGAATCAGGTTGGCTTAAGTGTATGAT
GAAATAGAATGGCAGATGGCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCTGGATCC
TATAAACACCCAAAGTACTTGGATTGATCCTACTCTTGATCAAAGTAGGTATAGGTTGTG
AACACAATCTTCTCAAGTCATACATGATGCCATTCTTGACTGGGATTATGGACACCTAC
TTTCAAGATGTTGTATGAGGATACACTTAAAGGCTCTGAGTATGGACAGATTAAACAAA
ATACCGTTGGATATCCAGAGTTAGCTGAAGTTAGGCAGATTGTAATATATAAAAAAAAGT
GTATTAATGTCGCCTGTCACTCAGATTGGGCACATTATATCTCAAAGAAAATATAATGAT
GCTCTGCATGGCGTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA
CTAGATACAAATATCCTGCCCTGCTACCTGGTCTGCTCATGAGCTGGTCATGCTGTAGGA
ATGTCACATGATGAACAAACTGCCAATGTAGGGTAGGCTTAATTGCATCATGGCCTAGGA
CGCACTGGGTTAGCAATTGCAAGTTATCTCTTTAAACATATCTCTGGAGCAACA
TGTCTAAATAATATCCAGGACTAGGTTATGTGCTTAAGAGATGTGAAACAAAATTGTGGAG
GACAATGAGGAATGTGACTGTGGTCCACAGAGGAGTGTCAAGAAAGATCGGTGTGCCAATCA
AATTGTAAGTTGCAACCAGGTGCAACTGTAGCATTGGACTTGTGTCATGATTGCGTTT
CGTCATCTGGATACGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAAGAGTACTGCGAC
GGGAATTCAAGTTCTGCCAAATGACGTTATAAGCAGGATGGAACCCCTGCAAGTATGAA
GGCCGTTGTTCAAGGAGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTGGACCT
GATGCCATGGAGGCTCTAGTGAGTGTATGATGCAGTTAACTTAATAGGTGATCAATTGGT
AACTGTGAGATTACAGGAATTGAAATTAAAAAGTGTGAAAGTGCAAAATTCAATATGTGGC
AGGCTACAGTGTATAATGTTGAAACCATCCCTGATTGCCAGAGCATACGACTATAATTCT
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGCACAGGCTATCATCTATCCATGAAACCC
ATGGGAATACCTGACCTAGGTATGATAATGATGGCACCTCCTGTGGAGAAGGCAGGGTATGT
TTTAAAAAAATTGCGTCAATAGCTCAGTCCTGCAGTTGACTGTTGCCCTGAGAAATGCAAT
ACCCGGGTGTTGCAACAAACAGAAAAACTGCCACTGCATGTATGGGTGGGCACCTCCATT
TGTGAGGAAGTGGGTATGGAGGAAGCATGACAGTGGGCCTCCAGGACTGCTCAGAGGGCG
ATTCCCTCGTCAATTGGGTGTGTCATCATATAATGTTGCCCTATTATTAATCCTTCA
GTGGTTTGTGTTTCCGGCAAGTGATAGGAAACCACCTAAACCCAAACAGGAAAAATG
CCACTATCAAAGCAAAAATGAAACAGGAAGAATCTAAACAAAATGTAACAGGAAGAATCT
AAAACAAAATGGACAGGAAGAATCTGAAGCAAAACTGGACAGGAAGAATCTAAAGCAAA
ACTGGACAGGAAGAATCTAAAGCAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG
AAACAAAAAAAGTAACCGGCAATCCATACTCATTAGTAACACAGGCTCATTATTAACCA
GCTAATCATTATCAAAGGCTTCCATTCTCTCCAAATATTTTACTTTAATTTC
ACAAGTTTGTGATCAGCAAATAACAGCATTCTGTTGGAAACAAAAA

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FIGURE 204

MRSVQIFLSQCRLLLLVPMLLKGLEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS
YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDHPYIPKDCNYMGSVKESLDKATI
STCMGGLRGVFNIADKYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDEIEWQMAPYENK
ARLRDFPGSYKHPKYLELILLFDQSRYRFVNNNLSQVIHDAILTGIMDTYFQDVRMRIHLKA
LEVWTDFNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSGKVCSEL
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNCIMGSRTGFSNC SYISF
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDCGSTEECQKDRCCQSNKLQPGANCSI
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTPCKYEGRCFRKGCRSRY
MQCQSIFGPDAMEAPSECYDAVNLI GDQFGNCEITGIRNFKKCESANSICGRLQCINVETIPD
LPEHTTIISTHLQAENILMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCSVSSVLQ
FDCLPEKCNTRGVCNNRKNCMYGWAPPCEEVGYGGSIDSGPPGLLRGAIPSSIWVSIIM
FRLILLILSVVFVFFRQVIGNHLKPQEKMPLSKAKTEQEESKTKTVQEEESKTGTQEESEAK
TGQEEESKAKTQEEESKANIESKRPKAKSVKKQKK

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 684-705

N-glycosylation sites.

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

N-myristoylation sites.amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,
758-764, 767-773**Amidation site.**

amino acids 69-73

Disintegrins proteins

amino acids 429-479

EGF-like domain proteins

amino acids 650-662

Neutral zinc metallopeptidases, zinc-binding region proteins

amino acids 335-345

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FIGURE 205

CGGACGCCTGGCGGACCGTGGCGGACCGTGGGGAAAGGTTGAATGGGTAGAAGGCCCTG
TTGTGGAGGGAAACCACCCATCCTCCTGCCTCCCACCACCATCATCCTGGCTGGACGGAG
AGGGTGACGGGGCTGGGAAGGGGCAGCTCATGTTAGGTTCCAGGAGGGCTACCTGTTGA
CTGTCCTTGCAAGGAAGAAAACACCTGAGTGAACAGATGTCCAGCTCCAGGTGCCTGCC
AGATGCCAGAACACACCTCTGAAGAGTGACAGTGCTGGAGCATGGTTCTGCACACCT
GGAATGACTGGAACCCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA
ACAGAAGGCTGTGGACCACCTGTCGAGATGGAGAAGTCCTCTGAGGCTATCAAACACGGAC
CAGGCCATGAGACCCCCGATGACCATCCCTGAATTTTCGAGAGTCAGTCAACCGATTGGAA
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAGTGGAAATTCTGAATTCAACAGTACT
ATGAGGCTTGTGGAAGGCTGAAAATCCTGATCAAGCTGGTTGGAGCGTTCCACGGAG
TTGGTATCCTGGGTTTAACTCTGCAGAGTGGTTACTGCTGTTGGGCCATCCTAGCCG
GGGGCTTGTGTTGGTATTTATGCCACCAACTCTGCCAGGCTGTCAATATGTCATCACTC
ATGCCAAAGTGAACATCTGCTGGTGAAGATGATCAACAGTTACAGAAAATCCTTCGATTC
CACAGAGCAGCCTAGAGCCCTAAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAAC
ACAACCTGTACTCTGGGATGATTCATGGAACCTGGCAGAAGTATCCCTGACACCCAACTGG
AGCAGGTATCGAGAGCCAGAAGGCAATCAATGCCAGTGCCTCATCTACACTTCAGGGACCA
CAGGCATACCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA
CAAAGGACTTAAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCACTCAGCCATA
TTGCAGCACAGATGATGGACATCTGGTACCCATAAAGATTGGGCGCTCACATACTTGCTC
AAGCAGATGCTCTCAAGGGCACCTGGTAAGTACTCTAAAGGAGGTAACACTGTCTCA
TTGGAGTGCCTCAAATTGGGAGAAGATACTGAGATGGTGAAGAAAAATAGTCCAAGTCCA
TGGGCTGAAGAAGAAGGCATTGTTGGCAAGAACATTGGCTCAAGGTCAACTAAAAAA
AGATGTTGGGAAATATAACTCCCGTAGCTACCGCATGGCTAAGACTCTCGTGTTCAGCA
AAGTCAAAGACATCCCTGGCTGGATCACTGTCACTCTTATCAGTGGACTGCGCCCCCTCA
ACCAAGAGACTGCCGAGTTCTTCTAACGCTTGGACATACCTATAGGCAGGTTATGGGTG
GTGAGAGCTCGGGACCCCACACGATATCCAACCCAGAATAACTACAGGCTTCTAACGCTG
AGATCTTGACTGGGTGAAGAATATGCTGTTCCAGCAGAACAGGATGGCATTGGGAGATCT
GCCTCTGGGTAGGCACATCTCATGGCTATCTGGAAAGTGAGACTGAAACTACAGAGGCC
TCGATGATGAAGGCTGGCTACACTCTGGGATCTGGGCCAGCTGGACGGCTGGGTTCT
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAGACTGCTG
CTGTTGAGACCTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA
AACTGAAGTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC
CTCTGGACAAGCTGAACCTCGAGGCCATCAACTCTGTCGGGCTGGCAGCCAGGCATCCA
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGCTACAAGGCCATCCAGCAAGGCATCA
ATGCTGTGAACCAGGAAGCCATGAAACATGCACAGAGGATTGAAAAGTGGGTATCTGGAGA
AGGACTTTCCATCTATGGTGGAGAGCTAGGTCAATGATGAAACTTAAGAGACATTTG
CCCAGAAATACAAAAACAAATTGATCACATGTACCACTGCTTCAGTGAATGCTG
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAATGCTG
AAGCTCTCCCTGCTGTTTAAGAAGCCACATTCCCATGGTCAGTTCTGATTG
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTCAAAGCAATAAAACT
TCTTCTAAGGACCTCAAGTCATGACTCCAGGGAAAGCTATTGGGAAGTCTACT
CCTGATTTACAAGAAAGACCTGAACCTGTTGGCTCCATTGATTG
TCAGACATTAGAAGAAAAAGCCTCACAGATTGAAGAACTGGACCCCCAAATCAACTCAC
GCCTGGAGCAACTGGGAAACCCTTCCAATAAGTCCTGATAATAAGCACTTCAGGGT
AAAAAA

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FIGURE 206

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAAKSLIKGLERFHGVGILGF
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQLQKILSIPQSSE
PLKAIIQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTS GTTGIPKG
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK
GTLVSTLKEVKPTVFIGVPQIWEKIHEMVKKNSAKSMGLKKAFVWARNIGFKVNSKKMLGKY
NTPVSYRMAKTLVFSKVKTSLGLDHCHSFISGTAPLNQETAEFFSLDIPIGELYGLSESSGP
HTISQNQNYRLLSCGKILTGCKNMLFQQNKGIGEICLWGRHIFMGYLESETETTEAIDDEGW
LHSGDLGQLDGLFLYVTGHIKEILITAGGENVPPIPVETLVKKIPIIISNAMLVGDKLKFLS
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE
AMNNAQRRIEKWVILEKDFSIYGGELGPMMKLKRHFVAQKYKKQIDHMYH

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 65-86

N-glycosylation site.

amino acids 196-200

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 282-286

Tyrosine kinase phosphorylation sites.

amino acids 547-555, 608-616

N-myristoylation sites.amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

Putative AMP-binding domain signature.

amino acids 177-189

Putative AMP-binding domain proteins.

amino acids 173-190

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FIGURE 207

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FIGURE 208

MAYRVLGRAGPPQPRARRLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVPAPRLSGSNHGSPLGKRLPQALIVGVKKGG
TRAVLEFIRVHPDVRALGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR
RIFNMSRDTKLIVVVRNPVTRAISDYTQTLSKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM
YVLHLESWLQYFPLAQIHFVSGERLITDPAGEGRVQDFLGIKRFITDKHFYFNKTKGFPCLK
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 102-106, 193-197, 235-239, 306-310

Tyrosine kinase phosphorylation site.

amino acids 296-305

N-myristoylation sites.

amino acids 51-57, 100-106, 121-127, 125-131

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 20-31

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FIGURE 209

CTTTCTTATCTGTGTACTCTTATCTCACTGTTCTATTTCTCCTCATTATTAAC
CTTCCTTACCTTTCTGAACCTCTAGGCCCTCTTCCAGAACTGGTGAAGACAAATG
AAACGGCCAAGATGGTAAGAAACAAGCCGCATTCTCCTGGGGAGACTGATAATTAAAAGG
TTTGTGTGTCAGAAACATTCCCAGCTTCATCACCAACCCTTCCTCCACCTCTGCCACTG
GAGACCACTTACATCCCGAACGCCAGCGCAGCTGAAGTCAGGAAACCATGCATCACATTAG
CAGGAGCCAAGTGCAGACTTAAACTCCGTTCAACATGTGGATGCCAGAGAA**ATG**ACCTGT
CCAGACAAGCCGGGGCAGCTCATAAACTGTTCATCTGTCCTGTGCGTCCCAGGGTGCCT
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTCTGCTGGCACTGCGTGTGCC
ATCTACTTGGGCTTCTGGTGAGCCAGGTGGGGAGGGCCTCTCCAGCATGGACAGGCCGCT
GAGAAGGGGCCACATCGCAGCCGCACACCGCCGAGCCATCCTCCCTGAGATAACCCCTGGAT
GGTACCCCTGGCCCCCTCCAGAGTCCCAGGGCAATGGGTCACTCTGCAGCCAATGTGGTGTAC
ATTACCCCTACGCTCCAAGCGCAGCAAGCCGGCAATATCCGTGGCACCGTGAAGCCAAGCGC
AGGAAAAAGCATGCAGTGGCATCGCTGCCAGGGCAGGAGGCTTGGTGGACCATCCCTT
CAGCCGCAGGAAGCGCAAGGAAGCTGATGCTGTAGCACCTGGTACGCTCAGGGAGCAAAC
CTGGTTAAGATTGGAGAGCGACCTGGAGGTTGGTGCAGGGTCCGGGAGTGCAGGCCGGGGC
CCAGACTTCCCTGCAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCAGAGCGCC
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGGCGGACAGCGCAGTGGCAGGG
CTCCGGCTGTGCTCTAGGAGCGGAGCCGTTGGTGCAGGGGGGGCAGCTGGC
GCTGTGCTCCGCTGTGGCCCTAGCCCCCTGAGGCTCTCAAGCAGCCCTGGACATGAGTGA
GTGTTGCCTTCCACCTAGACAGGATCTGGGCTCAACAGGACCCCTGCCGTCTGTGAGCAGG
AAAGCAGAGTTCATCCAAGATGGCGCCCATGCCCCATCATTCTGGATGCATCTTATCT
TCAGCAAGTAATGACACCCATTCTCTGTTAAGCTCACCTGGGAACCTATCAGCAGTTGCTG
AAACAGAAATGCTGGCAGAATGGCGAGTACCCAGCCTGAATCAGGTTGACTGAAATACAT
CATCATGAGTGGTCCAAGATGGCACTCTTGATTTTGTACAGATTATAATCGCTTAGAT
ACAAATTGCTGTGGATTCAAGACCTCGCAAGGAAGATGCCGTGTACAGAATGGATTGAGGCC
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCAGGAGCATGACCCAGG
CATTGGTTTTATAGACAACAAGGTTCTTGACAGGAGTGAAGATAACTAAACTTCAA
TTGTTAGAAGGCATCAAAGAGTTCCAGCTCTGCACTTCTGTTGAAGAGCAGCAGC
CGGCAGAAACTTCTCAGTCTGTGTTCTGATAAAGTGTATTGGAAAGTCAAGGAGGTAGA
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCTTACCTATATC
AATGCACACGGGGTCAAAGTATTACCTATGAATGA**TGA**CAAAAGAATCTCTGGCTAGGGT
TTAGATATATTATGCATTTGGTTTGTAAATCAAGCACATCAACCTCAAGCCGTT
TAGCAATGAGGCAGTGTAGATGAATACGTAAGGTTAAATGACTTAAACCAAGTAGCTATAAAGG
GACTTAGCACTGTATGCATACTTAAAGGTTGAAAACAAACTACTTGAGAAATATTGT
TTATATTCTCTAACATCATGCTATGTCAGTCTGAACATCTGACAACAGAAATTCAAG
TATTATTCTAGCTAACATCATGCTATGTCAGTCTGAACATCTGACAACAGAAATTCAAG
GATACTGACTCCATTAATAAACCATATTGTCAGGCTTTGACTGTTCTGACCAAAACTAAT
GGGAACAATTCTGACGTTCTGCTGATTGTTAACATAGAGCAGTCTCACACTACCC
TGAGGCAACTCACATTGAAACACTGAGGCTTACAGCCTGCAAGAGCAGAGCTGACCATA
CATTAAACAGAAATGCTGGTTATTGCAAAATCACCAGTATATTCTATTGTCATAA
AAAATCAGTCATTAAAGTACAAGAATCATATTCCATTCTTTAGAAATTATTGTTG
TCCCTATGAAATCATTACATCTGACAATTATATGTTAAAGAGTTACTCTCTATTT
GGTCCAATTGTTACTAGTGGCTGAGAAATTAAATAATTCTAAAGTATGAAGTTACCTATCTG
AAAATGTAACAGAGTATCTTAAATGGATGTCCTTAAAAATTGTTACTTTAC
CAACAATGTAATATAATTGTTATTGTTAACATAGTGAATTCTTAAATGTTACT
ATGTAACATTATTAATTGTTAACATGGTTACTGCCAGATATTGAGAAATGGTTCAAATAT
TGAGTGTGTTCAATAA

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FIGURE 210

MTCPDKGQLINWFICSLCVPRVRKLWSSRRPRTRRNLLGTACAIYLGFVSVGRASLQHG
QAAEKGPHRSRDTAEPFPEIPLDGTAPPESQNGSTLQPNVVYITLRSKRSPANIRGTVK
PKRRKKHAVASAAPGQEALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERPWRVLVRGPGR
AGGPDFLQPSSRESNIRIYSESAPSWSKDDIRRMRLLADSAVAGLRPVSSRGARLLVLEGG
APGAVLRCGSPCGLLKQPLDMSEVFHLDRLILGLNRTLPSVSRAEFIGDGRPCPIILWDA
SLSSASNDTHSSVKLTWGTYQQLLKQKCWQNRPVPKPESGCTEIHHHEWSKMALFDLQLIYN
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAALAHIIQRKHDPRHLVFDNKGFFDRSEDNL
NFKLLEGIKEFPASAVSVLKSQHLRQKLLQSLFLDKVYWESQGGRQGIEKLIDVIEHRAKILI
TYINAHVVKVLPMNE

Transmembrane domain:

amino acids 40-56

N-glycosylation sites.

amino acids 98-102, 289-293, 322-326

N-myristoylation sites.amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,
287-293, 484-490

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FIGURE 211

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGCCGCGCCGTGCTGCTGCTGC
TGCTGCTGTGGCTGCTCGCGTTCCCGCGCTAACCGGCCCGCGTCGGCGCTATTCGCCCTCCGACCCGC
TGACGCTGCTGCAGGCGAACACGGTGCAGCGCGGTGCTGGCTCCCGCAGCGCCTGGCCGTGGAGTTCTCG
CCTCTGGTGCAGGCCACTGCATGCCCTCGCCCCGACGTGGAAAGGCGCTGGCGAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG
CGGCCCTGTATCTGCCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG
GCTTCCCAGCTGTGAGGTTCTCAAGGCTTACCAAGAAGCGCTGGGAGCAGTATTCCAGTGGCTGGTCTG
ACGTGAGACGCTGCCGGAGAGGCTCATGGCCCTGGAGTCCCATCATGACACGTGGCCCCAGCCTGTCCCC
CACTGAGGCCCTGCCAAGCTGGAGGAGATTGATGGATTCTTGGAGAAAATAACGAAGAGTACCTGGCTCTGATCT
TTGAAAAGGGAGGCTCCTACCTGGTAGAGAGGTTGGCTCTGGACCTGTCCCAGCACAAAGCGTGGCGGTGCGCA
GGGTGCTAACACAGAGGCCAATGTGGTAGAGAAGTTGGTGTACCGACTTCCCCTTTGCTACCTGCTGTTCC
GGAATGGCTCTGTCTCCCAGACTCCCCTGCTCATGGAATCCAGGTCTTCTATACCCTTACCTGAGAGACTCT
CTGGGCTACCAAGGGAGGCTGCCAGACCACAGTGCACCAACCACGTGCTAACAAAGATAGCTCCACTGTTGGA
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCACTACATCCTGCCGATAGAAGTGG
GCAGGGTCCCGTCTGGAAAGGGCAGGCCCTGGGGCCCTGAAAAAGTTGTGGCAGTGTGCTGGCCAAGTATTCC
CTGGCCGGCCCTTAGTCCAGAACCTCCTGCACTCCGTGAATGAATGGCTCAAGAGGAGAAGAGAAAATAAATT
CCTACAGTTCTTAAACTGCCCTGGACAGAGAAAGAGGGTGGCTTGTGCCAAGAAGGTGAACGGATTG
GCTGCCAGGGGAGTGGAGGCCATTCCGGGCTTCCCTGCTCCCTGTGGGCTCTTCCACTTCTGACTGTGC
AGGCAGCTGGCAAAATGTAGACCAACTCACAGGAAGCAGCCAAGGCCAAGGGAGGTCTCCAGGCATCCGAGGCT
ACGTGCACTACTTCTCGGCTGCCAGACTGCGTAGCCACTTCGAGCAGATGGCTGCTGCCCTCATGCACCCGG
TGGGGAGTCCCAAGGCCCTGTCCTCTGGCTCTGGCTAGGCCACAACAGGGTCAATGCTGCCCTGAGGTGCC
CCAGCGAGGACCCCCAGTCCCAAGGTGCAGTGGCCACCCCGTGAACCTTGTCTGCCCTGCCAACATGAACGCC
TGGATGTGCCCGTGTGGGACGTGGAAGCCACCCCTCAACTTCTCAAGGGCCACTTCTCCCAAGCAACATCATCC
TGGACTTCCCTGCACTGGTCAGCTGCCGGAGGGATGTGAGAATGTGGCAGGCCAGAGGCTGGCGATGG
GAGCCCTGGAGTGGAAAGCCGAATTCAACTCTGGACCTGGCAACTTCTGGCTAGGATGATGAAGTCCCCAACAAACA
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTCGACCCCCGAAGCTGCACCCCTGGCCTCAGAGCTGCAC
CAGGCCAGGAGCCTCTGAGCACATGGCAGAGCTCAGAGGAATGAGCAGGAGCAGCCCTGGCAGTGGCACT
TGAGCAAGCGAGACACAGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCCTCTGGGGCCCTTGG
AGGTCAAGCGCGTGGCCGCAGCTCCAAGCAGCTGGTCAACATCCCTGAGGGCCAGCTGGAGGGCCAGCTGGAC
GGGGCCAGGCCAGTGGCTGCAGGTGTGGAGGGGCTTCTTACCTGGACATCAGCCTCTGTGTGGGGCT
ATTCCCTGCTTCTCATGGGCTGCTGGCATGTACACCTACTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG
CTGGCACCCTGAGCCTGAACCACCTGGGAGGGAGGAGGGAGCTGCATCTAGGCACCTCAAGGCC
CCTGACCCCATTCCCTCCCTGCCACCCCTTGCTCCTGTCTGGCTAGAAGTGTGGAAATTCAAGAAAACGAG
TTGCTCAGTGAAGCTTGGGTTGCTAGGACAGAGAGCTCTTGACACAAAAGACAGGAGCAGGGTCCAGG
TTCCCTGCTGTGCAGGGAGGGCAGCCCCGGCAGTGGCATAGGGCAGCTCAGTCCCTGGCCTTGTAGCACCAC
ATTCCCTGTTTTCAGCTTATTGAGTCTGCTCATTCTCACTGGAGCCTCAGTCTCTCTGCTTGTCTGG
CCTCAACTGGGCAAGTGAAGCCAGAGGAGGGTCCCCCAGCTGGGTGGCTGGAATGGAACCTCTCAACTAGCTGC
TGGGGCTCCGCCACCTGCTCCCTCCGGACAATGAAGAACCTTTGCACCCCTGGAGGAAGGACCACCCGG
CCCTCATGCCCTGGCCAGCCTCCAGCTCAGACCTCTGGGTGGGTTGGCTTGTAGGGTGGAGTGGCTTGTGG
TTCTGGAAGTCGTGCTGGCTCCAGGTGAGGCAAGGCCATGGTGGCTGAGGAGTGGCTTGTAGCTGCAGGAGAAG
GGGACCTGACGAGTGGTGGCATGGAGGAGTGTGGTCTCTAGTGCCTTGCCTGGCTTAGCTGCAGGAGAAGA
TGGCTGCTTCACTTCCCCCATTGAGCTCTGCTCCCTGTAGGCTGGTCTTGTCTTGTCTTTTATTGGTCTC
CAAGATGAATGCTCATTTGGAGGGTGCAGGTAGAAGCTAGGGAGGGAGTGTCTCTCTCCAGGTTAC
CTTCAAGTGTGCAGAACGTTAGAAGGGCTGGCGGGGGCAGTGCCTTACACATGCTTGTGATTCCCACGCTACCC
GCCTTGGGAGGTGTGGAATAATTATTTGTTAAGGCA

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FIGURE 212

MRCNSGSGPPSLLLLLWLLAVPGANAAPRSALYSPSDPLTLQADTVRGAVLGSRSAWV
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL
MESRSFYTAYLQRLSGLTREAAQTTVAPTANKIAPTVWKLADRSKIYMADLESALHYILRIE
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR
KEGAVLAKKVNWIGCQGSEPHFRGFPCLWVLFHFLTVAARQNVDHQSQEAAKAKEVLP
YVHYFFGCRDCASHFEQMAASMRVGSPNAAVLWLWSSHNRVNARLAGAPSEDQFPKVQWP
PRELCSACHNERLDV рVWDVEATLNFLKAHFSPSNII LDFAAGSAARRDVQNVAAPELAMG
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGEPPEASRPPKLHPGLRAAPGQEPP
NEQEQLGQWHL SKRTDGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGR
RGQWLQVLGGGFSYLDISLCVGLYSLSFMGLLAMYTYFQAKIRALKGHAGHPAA

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 705-728

N-glycosylation sites.

amino acids 130-134, 243-247, 575-579

Glycosaminoglycan attachment site.

amino acids 6-10

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 644-648

N-myristoylation sites.amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

Thioredoxin family proteins

amino acids 62-78

FIGURE 213

GCACGAGGCCGACTTCCAGACCATCTACAAC TGACGGCCTGGAACAGCTTCGGCTCCGACAC
TGAGATCATCCGGCTCAAGGAGCAAGGTTGGAAATGAAGTCGGGAGCCGGCTGGAAGCAGA
GTCTGTGCCGATGCCGT CATATTGGGTTGGCGTAGGAGCTGGTGTGGCCTCCTCGTCCT
TATGGCAACCATCGTGGC TTCTGCTGTGCCGTTCCAGAGAAATCTCAAAGGTGTTGTGTC
AGCCAAAATGATATCCGAGTGGAAATTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGTGAATTCCAGCAAGACTCAGTCCT
GAAACAGCTGGAGGTCTCAAAGAACAGGAGAAAGAGTTT CAGAACCTGAAGGACCCCACCAA
TGGCTACTACAGCGTCAACACCTCAAAGAGCACC ACTCAACCCGACCATCTCCCTCTCCAG
CTGCCAGCCCCGACCTCGCTGCCTGCCGTAAGCAGCGTGTGCCACAGGCATGTCCCTCACCAA
CATCTACAGCACCC TGAGCGGCCAGGGCCGCCTCTACGACTACGGCAGCGTTGTGCTGGG
CATGGG CAGCTCGTCCATCGAGCTTGTGAGCGGGAGTCCAGAGAGGCTCCCTCAGCGACAG
CAGCTCCTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCGGCAAGCAGGATGGCTA
TGTGCAGTTCGACAAGGCCAGCAAGGTTCTGCTTCCCTCCACCACCTCCAGTCCTCGTC
CCAGAACTCTGACCCCCAGTCGACCCCTGCAGCGGCGATGCAGACTCACGTCTTAGGATCACA
CACCGCGGGTGGGGACGGGCCAGGGAAAGAGGT CAGGGCACGTTCTGGTTGTCCAGGGACGAGG
GGTACTTGCAGAGGACACCAGAATTGCCACTTCCAGGACAGCCTCCAGCGCCTCTGCCAC
TGCCTTCCCTCGAAGCTCTGATCAAGCACAATCTGGTCCCCAGGTGCTGTGCTGCCAGAGGT
GGGCGGGTGGGGAGACAGACAGAGGCTGCCGTGAGTGCCTGTGCTTAGTGCCTGGACACCCG
TGTCCCCGGCCCTTCTGGAGGCCCTCTACCA CCTGCTCTGCCACAGGCACAAGTGGCAG
CTATAACTCTGCTTTCATGAAACTGCCGTCCACTCTCTGGTCTCTGTGGCTCTACCCCTC
ACTGACCACAAGCTCTACCTACCCCTGTGCCCTGTGCTCCATACAGCCCTGGGAGAAGGGGA
TGACGTCTCCAGCACTGAGCTGCCAGAAACCCGGCTCCCACTGCTGCTCATAGCCA
TACCCCTGGAGGCTGACAAGCCAGAAATGCCCTGGCTAAAGGAGCCTCTCTCACCAGGCTG
GCCGGGAGCCCACCCCCAATTGTTGGTGTGCTACTCTGCAGTTCTGTCCCTTG
GACTTGATGCCGTGAACCTGCGGTGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA
GGGAGGGAGGAGGGAGCCGTGCTGACGGAGCACCTGCCGGGTGTGCCCTCTGGCTGTG
TGACCCAGCCTCCCCACCCACCTCCTGCTTGTGACTCCTCCCTCCCCCTCAGCACAATC
GGAGTTCATATAAGAAGTGCAGGGAGCTTCTCTGGTCAAGGGTTCTCTGAACACTTATGGAGAGA
GTGCTTCCCTGGGAAGTGTGGCGTTGAAGGGGCTGGAGGGCAGGTCTTAAGATGGCGAGACT
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTCAGTAAGGCTCCACGAGAAGA
GAGGAAGTATCTACACCTCAACCCCTCAGTCACCACCTGAAATAATGTTAGGGAAAAAAA

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FIGURE 214

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLGVVSAKNDIRVEIVHKEPASGREGEHSTIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCOPDLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSFLDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 150-154

N-myristoylation sites.

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 114-125

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FIGURE 215

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTCCCTGGTCCCTGCTATTGTCGGGGACG
ATTGCATGGGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTATTGGGCTGGCG
CCTGCTATTGCATTATAGACTGACTAGGGGAAGAAAACAGAACAGAAGGAAAAATGGCTGAGG
GTGGATCTGGGATGTGGATGATGCTGGGACTGTTCTGGGCCAGGTATAATGACTGGCTG
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGCTCGGATTG
GGACTGAAGCTGGAACCAGAGCTAGGCCAGGGCAAGGCCAGGGCTACCCGGCACGTGGG
CTGTCAGAAACGGCTCCCCAATTCAAGATGATACCGTTGTCCCCTCAAGAGCTACAAA
AGGTTCTTGCTGGTGGAGATGTCTGAAAAGCCTATATTCTGAAGCAGCTTAATTGCTC
TGGGTAACAATGCTGCTTATGCATTAAACAGAGATATTATCGTGTCTGGGTGGCTCCAA
TTGTCGCAAAGATTCTCAATACTCGGATCCCAGTTAACAGAGATATTATCGTGTCTGGGTGGCTCCAA
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTAAAGTATACTGAATCAAGTGTGTG
ATGACACAATCACTCTCGCTTGAACTCATCTGTGCAGCTTGGACTGAGATTGCTTACAA
ATATGACTGTTACTAATGAGTATCAGCACATGCTGCTAATTCCATTCTGACTTTTCGTT
TATTTCAAGGGAAATGAAGAACCAAACCTCAGGTTCTGAAACTCCTTTGAATTGGCTG
AAAATCCAGCCATGACTAGGAACTGCTCAGGCCAAGTACCATCTCACTGGCTCCCTCT
TTAATAAGAAGGAGAACAAAGAAGTTATTCTAAACTCTGGTATATTGAGAACATAAATG
ATAATTCAAATGGAAAGAAAATGAACCTACTCAGAACATCGGTGAAGGTTCACTTTTT
TCTTTTAAAGAATTCAAGTGTGTGCTGATAAGGTTCTGGAAATAGAAAGTCACCATGATT
TTTGGTGAAGTAAAGTTGGAAAATTCAATGCCAAACTGCTGAACATATGTTCCAAAGA
GCCAGGAAAACACCTGATTTGTAATTAGAACACACATTGAAACTATTCAATTTC
TCCACCTGTTATATGGTAAAGGAATCCTTCAGCTGCCAGTTGAATAATGAATATCATA
TTGTATCATCAATGCTGATATTAACTGAGTTGGCTTGTGTTAGGTTAAGATGGATAATGAATA
TCACRACTGTTCTGAAAACATGTTGCTTTATCTCGCTGCCTAGATTGAAATATT
GCTATTCTCTGCATAAGTGACAGTGAACCAATTCAATGAGTAAGCTCCCTCTGTCATT
TTCATTGATTTAATTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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FIGURE 216

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEKMAEGGSGDVDDAGDCSGARYNDWSDD
DDDSNESKSIVWYPPWARIGTEAGTRARARARARARAVQKRASPNSDDTVLSPQELQKV
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVLNN
LSVNAENQRRLKVMQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF
SAGNEETKLQLVKLLLNLAEVPAMTRELLRAQVPSLGSLFNKKENKEVILKLLVIFENINDN
FKWEENEPTQNQFGEGSLFFFKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 68-72, 189-193, 217-221, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-111

N-myristoylation sites.amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,
290-296**Amidation site.**

amino acids 29-33

FIGURE 217

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FIGURE 218

MAIAQLATEYVFSDFLLKEPTEPKFKGLRLEAVDKMVTCAVGLPLLLISLAFQEISIGTQ
ISCFSPPSSFSWRQAAFVDSYCWAAVQQKNSLQSESGNLPLWLHKFFPYILLFAILLYLPPLF
WRFAAAPHICSDLKIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES
HFKYPIVEQYLTKKNSNNLIIKYISCRLLTLIILLACIYLGYYFSLSSLSDEFVCSIKSGI
LRNDSTVPDQFQCKLIAVGIFQQLSVINLVVYVLLAPVVVYTLFVPFRQKTDVLKVYEILPTF
DVLHFKSEGYNDLSLYNLFLEENISEVKSYKCLKVLENIKSSGQGIDPMLLLTLNLGMIKMDVV
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQRLLDSSC

Transmembrane domains:

amino acids 37-55, 108-126, 216-232, 273-290

N-glycosylation sites.

amino acids 255-259, 338-342, 394-398

Glycosaminoglycan attachment site.

amino acids 357-361

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 61-67, 174-180, 251-257, 393-399

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 218-229

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FIGURE 219

CTGTGAGTGACACACGCTGAGTGGGTGAAGGGAAATGCTGGTGAATTCA
GTTGCTGTTAGTCACTCTGTCTTGCATTGCCAAGCACAAGCAATCTCCTCACCAAAA
GTTGTTACCCAAGGGAACATTGTCAGCTGTTGACGCTCTATATCAAAGCAGCATGGC
TCAAAGCAACGATTCCAGAAGACCGATAAAAAATACGATTATTAAAAAGAAAACAAAAA
AGCAGTTATGAAAAACTGTCAATTCAAGAACAGCTTCTGTGCTTCTTCATGGAAGACGTT
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTGTGGAGGACTTCATAGCCTA
GGCAGAAATTGAGCCACTGTATTCCCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA
GGATGAAAAGAATATTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGA
ATATTCTTCTTCCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAGCCAAGTACA
TTGATTTACAGTTATTTGAAATAACAATAAGAACTGCTAGAAATATGTTATAACAGTCTAT
TTCTTTAAAAACTTTAACATAACTGACGGCATGTTAGGTGATT
CAGAATAGACAAGAA
GGATTAGTAAATTACGTTGGATATAAGTTGTCACTAATTGCACATTCTGTGTTTC
AAATAATGTTCCATTCTGAACATGTTGTCATTACAAGTACATTGTGTC
AACTTAATTAA
AAGTATGTAACCTGAATTAACTCGTGTAAATTGTTGTTGAGTGGGATGTGGGGGTGGAG
GGGAAATGACAGATTCTGGAATGCAATGTAATGTTACTGAGACTAA
ATAGATGTTATGTAT
ATGATTGTC
GTTAAGTGTGTTGAAAATTGTTAATTATGCCAGTGTGA
ACTTAGTACTTAAC
ACATTGATTAAATTAAATTGGTTCTCA
AAAAAAA
AAAAA

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FIGURE 220

MLVNFILRCGILLVTLSLAIAKHKQSSFTKSCYPRGTLSQAVDALYIKAAWLKATIPEDRIKN
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLLESSQ

Signal sequence:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 68-71

N-myristoylation site.

amino acids 148-153

Interleukin-10 proteins.

amino acids 58-94, 74-102, 128-170

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FIGURE 221

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGAC**ATG**AGGCAGGCCGGCGGTGCCGCTCC
TGCTGCTGCTGTGTTGGTCTCAGAGGCCAAGGCAGCAACAGCCTGTGGTCGCCAGGA
TGCTGAACCGAATGGTGGCGGGCAGGACACGCAGGAGGGCAGTGGCCCTGGCAAGTCAGCA
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGAGCAGTGGTCCTGACGG
CTGCGCACTGCTTCCGAAACACCTCTGAGACGTCCCTGTACCAGGTCTGCTGGGGCAAGGC
AGCTAGTGCAGCCGGGACACACGCTATGTATGCCCGGGTAGGGCAGGTGGAGAGCAACCCCC
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCT
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATTTGAGACGGGCATGA
ACTGCTGGGTCACTGGCTGGGCAGCCCCAGTGAGGAAGACCTCCTGCCGAACCGCGGATCC
TGCAGAAACTCGCTGTGCCCATCATGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA
CCGAGTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCCCGGCTCGAGGAGG
GCAAGAAGGATGCCCTGCAAGGGGACTCGGGCGGCCCCCTGGTGTGCCCTCGTGGTCAGTCGT
GGCTGCAGGCAGGGGTGATCAGCTGGGTGAGGGCTGTGCCGCCAGAACCGCCAGGTGTCT
ACATCCGTGTACCGCCCACCAACTGGATCCATGGATCATCCCCAACTGCAGTTCCAGC
CAGCGAGGTTGGCGGCCAGAAG**TGA**AGACCCCCGGGCCAGGAGCCCTTGAGCAGAGCTCTG
CACCCAGCCTGCCGCCACACCATCCTGCTGGCCTCCAGCGCTGCTGTTGACCTGTGAG
CCCCACCACTCATTTGAAATAGCGCTCCTCCCTCTCAAATACCCTATTTATTT
ATGTTCTCCAATAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAA

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FIGURE 222

MRRPAAVPLLLL CFGSQR AKAATACGRPRMLNRMVGGQDTQE GEWPWQVSIQRNGSHFCGGS
LIAEQWVL TAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWS PSEEDLLPEPRILQKLAVPIIDTP
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDGGPLVCLVGQS WLQAGVISWGEG
CARQNRPGVYIRVTAHHNWIHRIIPKLQFQP ARLGQK

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 55-58, 79-82

Casein kinase II phosphorylation sites.

amino acids 121-124, 165-168, 167-170, 248-251

Tyrosine kinase phosphorylation sites.

amino acids 78-86, 197-203

N-myristoylation sites.

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

Amidation site.

amino acids 219-222

Serine proteases, trypsin family, histidine active site.

amino acids 71-76

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FIGURE 223

CAAGATGTGGACAGCTTGTGCTCATTTGGATTTCTCCTTGTCTTATCTGAAAGCCATGC
GGCATCCAACGATCCACGCAACTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAAGAGGAA
TGCATCTGTGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTCTCC
TGTACATTGACCAAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAGGA
CACAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC
CATTGCTCCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG
TATGACTGTGGCCTCCAGTGCTCCCACGACTGCAGCCTCCAGTACAACGTGTCAGCTCCATTGC
TCCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCAGCAGCTCCATGACACTGCACTCCC
CGCGCCACGTCCACTTCCACAGGGCGGACCCGTCCACTACCGCCACTGGCATTCCATCTCT
CAGCACAGCCCTCGCACAAGTGCCAAGAGAGCAGCGCGTGCCAAGAACAGCAACCCGGCCAC
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG
TCCAAGTCCTTCCAAGCACATGCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC
CCAAGCACAAGGTCCCATTAGCCAGGTGTAGTGACCAGCCTGTGGTTAACACAACAAATAA
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCGGCCCCACCCCCACAGTGGTGACAC
CACCAAGGCACAAGCCAGGGAGCCAATGCCAGCCCAGTGCCAGTACCTCACACCAAGCCAAAT
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC
CGCTGGGCCAGGCACATCCCAGGGCACCGGAGCAGGTAGAGACTGAAGGCCACACCAGGTACTGA
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTCCA
GCCCAAGCACCCAGGCCAGTACATGGTGGTACCAACTGAGCCCTCACCCAGGCCGTGGTAGA
CAAACCTCTCCTCTGGTGGTGTGTTACTCAGGGGTGACCCCTTCATCACAGTCTGGTTTT
GTTTGCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAAT
CAACGGGATGTATGCCAGACTCAGAAATGTGAGGGGGGCGGGGGCTGGCGGGAGGCCTGGCCC
CTTCCTCGTCTTCTTGCCTTGAGACCAACCAAGTGCTTCAAATTCTTGGTGCA
ATTGAGGAGATATGCCAGATGCTAAACACATTAAATTGCTGTCAGATTAATTCCATGATCAC
TAAAGAGTTGCTGCTTTTCAATTATTTGAAATGATTCTGTGCCAGGAGCAGCTGG
GGGTCCACCTCAGGGTGGGCGGGCAGGACCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA
ATTAAAGTACTGACTGCTCGCCA

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FIGURE 224

MWTALVLIWIFSLSLSESCHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDTMAAASPVT
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRSPSKHMPSDTAASPVPPMRPQ
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTKAQAREPTASPVVPVHTSPIP
EMEAMSPTTQPSPMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP
STQGQYMVVTTEPLTQAVVDKTLVVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN
GMYADSEM

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 396-420

N-glycosylation sites.

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

Casein kinase II phosphorylation sites.

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

N-myristoylation sites.

amino acids 68-73, 354-359

Aldo/keto reductase family putative active site signature.

amino acids 195-210

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FIGURE 225

GGAAAGGCGCTCAAGGTGCGCGGCCCGGGCGCGCTACTGGGGCGCCCTCCGCGGTGGCAGC
GCGCCAGGGATCGGCCTGGCAGCCGCGGGCGCGAAGGCTGCCTTCCTACGGCCCC
CTCGCTTCCTCCGGCACGGCGAACGGAGATTCCCTCTCGGGAAACTACGC GGATCCTTT
CGGGGATCCTCGCCCCGCCAGTTCTCCGCCCCCTCCCTTGCTGGGCGCCTGGCTGGC
CCGGCGAGGGGAGGGAGGCTCTGGCAGCCTGGCAGGGAGGCGGGGGCGGGAGCCGCT
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCCCTAGCCCTGCGACCCCCAGCGCGTCCCG
GCCTGCGCTCCGCCCGCGCAGCGCACGATGCTCTGCCGGACGCGCACGCCAACCGC
CGACGCCCGAGCCGTGCAGCATCCGGCTCCGCCGGCAGGTAGAGCCGCCGGCAGCTCC
TGCGCCTTTCTACTGCACTGTCCCTGGCTGCTCAAAGAGATCTAGCGCTACCGACTTCT
CTGGTTACCTAACCAAACCTCCTGCAAAACCACACCACCTATGCCGTGATGGGACTATTGA
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGCATTATGGCAAGATTACC
AAATGTGTAGTCCCAGAAGCCTGCCTCCAGAGGGAAAGACAGCTAACCTGTGAGGCCA
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCCAGCGGGCCTGCCACCTCCTGGTCAATA
GCCGTGTTTGGACCTGACCTTGTCCAGGAAGCAGTAATACCTCCTGGTCTCCTTAAAT
GCCAACCTAATGAATTAAAAAACAAAACCGTGTGTAAGACCAGGAGCTGAAACTGCACTGCC
ATGAATCCAAGTTCCCTAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTCGATTGCTTACTCAGCTTGCAAG
TCCTATCCGAAGGTGCTATGGGAAGCAGAGATGCAAATCATCGTCAACAATCACCATTG
GAAGCCCTTTGCCAGGCAGGTGAAAAAAATACCTACTGTGACCTACGCATGTGTTCCAAGA
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAACCTCTTGAGCAGAAAGATG
GTGAATATGGTATAAAACTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTG
TTAGCAACTCTGGCAGCCTTGCTTACATTAGAGCCCACCCAGAGAGAGCTGCCCTGCTGT
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCCCTGGTCATCAGAGAGTCT
GTGCCAAGGACTTCCCGACTTGCAGCTGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTTGAGTCTGATTCCCAGGGG
AACTGTGGGTTCTGTAGGACTTCATATCCTATATACAGTCCATAGAAGCTGCAGAGCTCG
CAGAAAGGATTGAGCGAGGGAGCAAATCATTAGGAAATATGGATGAACAGTGGTTGGACA
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTTGAAAACCACATGCATCTGATGCGATCGCA
CTTTCTGAAGAAGGAAGGATCCAAATGCCCTCCAGTTCTGGTCACCTGTACCTTCTATGA
AGGAGAATTCGTCATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATTTCAA
GCTGTTCTAGCACATTCCAAAATAATGAGGAGGGAGGAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

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FIGURE 226

MLLPGRARQPPTPQPVQHPGLRRQVEPPGQLLRLFYCTVLVCSKEISALTDFSGYLTKLLQNH
TTYACDGDYLNLQCPRHSTISVQSAFYGQDYQMCSSQKPASQREDSLTCVAATTFQKVLDECQ
NQRACHLLVNSRVFGPDLCPGSSKYLLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA
TYGRRTQERDICSSKAERLPPFDCLSYSALQVLSRRCYKGQRCKIIVNNHHFGSPCLPGVKKY
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPSGSKVLRKDGILVNSLAAFAYI
RAHPERAALLFVSSVCIGLALTLCALVIRESAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTSLPRNMGQFY

Transmembrane domains:

amino acids 32-49, 322-343

N-glycosylation sites.

amino acids 62-66, 165-169

Tyrosine kinase phosphorylation site.

amino acids 280-287

N-myristoylation site.

amino acids 302-308, 333-339, 428-434

Amidation site.

amino acids 191-195

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FIGURE 227

GGCACGAGGTGGAAGGGCTTTACAAACAGATTGCTGGCCCCACCCCCCAGAATTCTCATCA
GGAGTGGGCAAGACCAATCATTGCATTCAGACAAGTCCCAGGAGCTGCAGCTGCTGGCCC
TGGAACCACACTTGAGAACCACTGCTTAGACCAAACACCAAAGGAAGATGCAGGCCACCTC
CTTACATGTACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGCTAGGAGTGAAGCGTGTCA**CCATGG**
TCAGCTCATGGCCAGCCAGGAAAGCCTCTGCTGTGCGTCTGTGCAGTTCTTGTCTCCCT
GGAGGACTCTGGATGCCGTGATCTTGGCCAGGAGACCAGGTGCCTGGTCCCTCCTGG
AGGGGACAAGTTACACACCCCCAGCCCCATTTCACCAACTCTACATGCCTGGAGAAC
TTCTACATGTTGGCTGCCCTTCCCTATTCAGCAGTGCCAGTCCTGCTTATAAACCTGA
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCAATGTTGT
TGAGGCCAGATGGATTCCCTGGAAGCAGCTGGCCATGGATG**TGAGTC**CACAGTATTCTAGA
AACAGAGAAGAGGTCTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAACATACCCCT
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTCATGTGCTAGGGGCATGATAATGATAATAA
AGGAATTGTATCTAGGACTAA

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FIGURE 228

MVSSWPARKASLLCVCAVLVLPWRTLGSPIVARRPGAWVPSWKGTSYTPQPHFPTNFYMPWE
NLLHVGCPPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLAAGPWM

Signal peptide:

amino acids 1-27

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 8-12

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FIGURE 229

GGGAAGGGATGCAAGGAAGCCCTCCGGCGTGCCTCGAGGCAGGAGACAGCGTCCGCTGA
AAATGTGTGTCATGACATGCAAGCTCAGTGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT
CCGGACCTGGATCATGAAGGTGTGGAGAAGACTCTTCTGGGTGCTGTTCCGCTCTCC
CTGGCGGTGCAGGCTGTGGAGCAGGAGGTGGCGCAGCGTGTGATCAAACACTGCACCGCGG
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGTCCGGGACAGCTGCAGGAAGCTCTCAGG
GCTTCTCCGCCAGAAGAATGCAGTTCTGAACAAACTGAAAACGTCAATTGGAGCAGTGGAGAA
AGACGTGGCCTGTCGGATGAAGAGAAACTGTTCAGGTGCACACGTTGAAATTTCAGAA
AGAGCTGAATGAAAGTGAAAATTCCGTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCCTGGAGGCCCTGAG
AGAGGCTGCAATAAAGGAAGAACAGAATATATGGAACATTCTGGCAGCAGAAAAACATCAAGT
TGAAGCCCTAAAAATATGCAACATCAAACCAAAGTTATCCATGCTGACGAGATTCTGTA
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTGACGACAA
TAAATCAGTCAAGGGGTCAATTGAGGCAGTTCTGAGGGTGGAGGAAGAGGCCAATT
TAAGCAAAATATAACAAAAGAGAAGTGGAGGATGACTTGGGCTTAGCATGCTGATTGACTC
CCAGAACAAACCAGTATATTGACCAAGCCCAGAGATTCAACCATCCCACGTGCAGATCACCA
CTTATAAAGGACATTGTTACCATAGGAATGCTGTCCTGCCTTGTGGCTGGCTATGTACAGC
CATAGGATTGCCTACAATGTTGGTTATATTATTGTGGTACTTCTGGGACCTTCAGGACT
AAATAGTATTAAGTCTATTGCAAGTGGAGACATTAGGAGAATTGGGGTGTGTTTACTCT
TTTCTTGTGGCTTAGAATTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTCTTACA
AGGGCGTGTACATGACACTGTTAATGATTGCATTGGCTGTGGGGCATCTTGC
GATCAAACCCACGCAGAGCGTCTCATTTCCACGTGTCTGCTTGTCAAGCACACCCCTCGT
GTCCAGGTTCCATGGCAGTGCTCGGGTGACAAAGAAGGCACATTGACTACAGCACCGT
GCTCCTCGGCATGCTGGTACGCAGGACGTGCAGCTGGGCTCTCATGGCGTATGCCGAC
TCTCATACAGGGGGCGCCAGTGCATCTTAGCATTGCGTGGAAAGTCTCGAATCCTGGT
TTGATTGGTCAGATTCTTTCACTAGCGCGGTTTCTTATGCTGTATAAGAA
GTATCTCATTGGACCTATTATCGGAAGCTGCACATGGAAAGCAAGGGAAACAAAGAAATCCT
GATCTGGGAATATCTGCCTTATCTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC
CATGGAGCTGGCTGTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGGTACCGA
GGAGATGCCACCTCCATCGAACCCATCCGCACCTGGCCTCGTCTCCTCAGGGCCCCGGTACCGA
AGGGCTCCACGTGTTCCCCACGTTGTGGCGTACGAGCTCACGGTGTGGCTTCCTCACCT
GTCAGTGGTGGTGTGAAGTTCTCTGGCGCGCTGGCTGTCTCATTCTGCCGAGGAG
CAGCCAGTACATCAAGTGGATCGTCTCGGGGCTTGCCTGGCAGGTCAAGCAGTTCTTGT
CCTGGGGAGCCGGCGCGAAGAGCGGGCGTACCTCTCGGGAGGTGTACCTCTTACTGAG
TGTGACCACGCTCAGCCTTGTGCTCGCCCCGGTGTGGAGAGCTGCAATCACGGAGTGT
GCCAGACCGGAGAGACGGTCCAGCCTCTGAATGGCTCGGAGATGATGGACCGTGGAAAGGGAAAG
CGTCTGTGGGAGTGAGCGCTTAGATGGCAGCAGCTGCTCCTCTGGGAAGCTCGCACCTG
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCGGCTTACAGAATA
TTCTGTCCTATTTAGAATTTCGGAGTAGTTATTGCACTGCTGTGATTATGTGCAAGTA
GACCCGGGACACTGCCTTACCGATCACCTGAATGTTGCTGGATGTGCCTTTTT
TTTCCCTGAAATTATTATTAAATTCTATTGTGAGTTCATGAGTCAGTTCATAGTTTTAGTAA
GAAGAAAATTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAA
TTGTTATTAAACATTCTGTAATATGAAGTTGTAATCCTGGCGTGGAGCTGGAAAGCTTACT
TTGATTCTAAAGCCTATGTTCTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAA
TGTAACTTAAATGAAATAATTGCAATTCTATTAGATATGCACTTAAATATTG
GTTTAAATCACAAGAATATGTATTCTTAATAAGATAATTGATCATGGTAAAAAAAAAA

FIGURE 230

MKVLGRSFFWVLFVLPWAVQAVEHEEVAQRVIKLHGRGVAAMQSRQWVRDSCRKLSGLLRQ
KNAVLNKLKTAIGAVEKDVGSLDEEKLFQVHTFEIFQKELNESENSVFQAVYGLQRALQGDYK
DVVNMKESSRQRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSMLEILEDVRK
AADRLEEEIEEHAFDDNKSVKGVNFEAVLRVEEEEANSKQNITKREVEDDLGLSMLIDSQNNQ
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLNSIK
SIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPCYMTLLMIAFGLLWGHLRIKPT
QSVFISTCLSSTPLVSRLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA
GASASSSIIVVEVLRILVLIGQILFSLAASFLLCLVIKKYLIGPYYRKLMESKGNKEILILGI
SAFIFLMLTVTELVDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIFFASIGLHV
FPTFVAYELTVLVFLTLSVVVMKFLLAALVSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR
ARRAGVISREVYLLILSVTTLSSLAPVLWRAAITRCVPRPERSSL

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,
576-598, 641-660

N-glycosylation sites.

amino acids 104-108, 174-178, 206-210, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 55-59, 673-677

Tyrosine kinase phosphorylation site.

amino acids 407-414

N-myristoylation sites.

amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,
442-448, 525-531, 530-536

Cell attachment sequence.

amino acids 404-407

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FIGURE 231

GAGAAAAACAAACAGGAAGCAGCTTACAAACTCGGTGAACAACGTAGGGAACCAAACCAGAGAC
GCGCTGAACAGAGAGAACATCAGGCTAAAGCAAGTGGAAAGTGGGCAGAGATTCCACCCAGGACTG
GTGCAAGGCGCAGAGCCAGCCAGATTGAGAAGAAGGCAGGGAGCTGGCTGGGGCAGCAGAGCTG
TAATGCTGCTGTTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGCAGCAGCC
CTGCCTGGACTCAGTGCCAGCAGCTTCACAGAACGCTCTGCACACTGGCCTGGAGTGCACATC
CACTAGTGGACACATGGATCTAAGAGAACAGGGAGATGAAGAGACTACAAATGATGTTCCCC
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGACAACAGTCAGTTCTGCTTG
AAAGGATCCACCAGGGTCTGATTTTTATGAGAAGCTGCTAGGATCGGATATTCACAGGGG
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTCATGCCTCCCTACTGGGCCTCAGCC
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC
AGCCATGGCAGCGTCTCCTCTCGCTTCAAAATCCTCGCAGCCTCCAGGCCTTGTGGCTG
TAGCCGCCCGGGCTTGGCCATGGAGCAGCAACCTGAGTCCCTAAAGGAGCAGCTCAAGG
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAAATCTACCACCCCAGGCACCTGTG
AGCCAACAGGTTAATTAGTCCATTAATTAGTGGACCTGACATGATAAGGTTGAGTATTATTAGATGGGAAGGGAAATT
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTATTAGATGGGAAGGGAAATT
TGGGGATTATTATCCTCTGGGGACAGTTGGGAGGATTATTATTGTATTATATTGAAT
TATGTAACCTTTCAATAAGTCTTATTGTGGCTAAAAAAAAAAAAAAA

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FIGURE 232

MLGSRAVMLLLLPWTAQGRAVPGGSSPAWTQCQQQLSQKLCTLAWSAHPLVGHMDLREEGDEE
TTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVGQLHA
SLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAHGAATLSP

Important features of the protein:

Signal peptide:

amino acids 1-21

Casein kinase II phosphorylation site.

amino acids 64-67

N-myristoylation sites.

amino acids 25-30, 81-86, 122-127

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FIGURE 233

CCCACCGTCCGGCCCTGTAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGTCTGCAGTGCAG
 CATTATGGGCCCTGACATGAATATGGAGTAGTTTCTCTAGCAAAGAGTA**ATGTGGGCCATGGAGTCAGGCCA**
 CCTCCTCTGGCTCTGCTCATGCAGCCTTGCGCCTCAACTGACTGATGGAGCCACTCGAGTCACTACCT
 GGGCATCCGGGATGTGCACTGGAACTATGCTCCAAAGGGAAAGAAATGTCATCACGAACAGCCTCTGGACAGTGA
 CATAGTGGCTTCCAGCTTAAAGTCTGACAAGAACCGGATAGGGGAAACCTACAAGAAGACCATCTATAAAGA
 ATACAAGGATGACTCATACACAGATGAAGTGGCCCAGCTGCGTGGTGGGCTCTGGGGCCAGTGGTGCAGGC
 TGAAGTGGGGATGTCATTCTTATTCAACCTGAAGAATTTCGCACTCGTCCCTATACCACCATCCACCTCATGGT
 CTCTCAGAGAAGGACTCTGAAGGTTCCCTATACCCAGATGGCTCCTCTGGCCACTGAAAGCTGATGACTCTGT
 TCCCCGGGGGAGCCATATCACAACGGACATTCCAGAAGGCCATGCACCCACCGATGCTGACCCAGCGTG
 CCTCACCTGGATCTACCATTCTCATGTAAGATGCTCACGAGACATTGCAACTGGCTAATTGGGCTCTCATCAC
 CTGTAAAAGAGGAGCCCTGGATGGAACTCCCTCTCAACGCCAGGATGAGACCATGATTCTTCCCTCT
 CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTCAGT
 GGACAAAGAAGATGAGACATTAGGAGAGCAATAGGATGCAATCAATGGCTTGTGTTTGGGAAATTAC
 TGAGCTGAACTGTTGCAAGAACGTTGCGACTTGGGACTGAGGAACTGGCTAACATCTTCCAGCCACCT
 AGCATTTCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTTGAGGAACTGGCTAACATCTTCCAGCCACCT
 TGTGACTGCTGAGATGGTGCCTGGGAACTGGTACCTGGTTATTAGCTGCAAGTGAACAGTCACTTCGAGA
 TGGCATGCAGGCACTCTACAAGGTCAGTCTGCTCATGGCCCTCCTGTTGACAGGCAAAGTTCG
 ACAGTACTTCATTGAGGCCATGAGATTCAATGGACTATGGCCGATGGGACTGATGGGAGTACTGGGAAAGAA
 TTTGAGAGAGCCAGGCACTTCAGATAAGTGGGACTTCCAGAAAGAGCTCCAGGCAATGGGAACTTACTGGGAA
 AGTGCATATGAAGCCTTCAGATGAGACATTCAAGAGAACAGATGCAATTGGAGGAAGTGGCATCTTGGGAA
 CCTGGGCCAGTCACTGGGCTGAGGCTGGTACACCATTGAGGTGGTCTCTACAACCGTGCCTCCAGCCATT
 CAGCATGCAGCCCCATGGGGCTTTAGAGAAAGACTATGAGGCACTGGTCACTGTCAGATGGCTCATCTTACCC
 TGGCTGGTTGCCAAGGCCATTGAGAAAGTCAACATACCCTGAGGCACTGGCTGGCACCTGGCTGGGACTGCTCA
 GGATCTGCTGCTGCTGAGGCACTGGTACCTCTGCTGAGATCCCATAAGAGAACACAAATTCTGGCTGGTGG
 CCCGCTGCTGGTGCAGGGCTGGTGCAGATGGCAAGCAGAAAGGGTGGATAAGAATTCTTCT
 TCTCTCACTGTTGGATGAGAACACAAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGCTATGTTGATTCCG
 ACTGCTTCACTGGGCTTCAAGACTCCAATCGATGCCATTAAAGGTTCTGTTCTCTAA
 CCTGCCAGGCTGGACATGCAAGGGTACACAGTGGCTGGCACCTGCTGGCTGGGACAGAGACTGATGT
 GCATGGAGTCATGTCAGGGCAACACTGTGCACTGGCATGAGGAAGGGTGCAGCTATGCTCTTCTCA
 TACCTTGTATGCCATCATGCAGCCTGACAACCTTGGACATTGAGATTATTGCCAGGCAGGCAGCCATCG
 AGAACAGGGATGAGGGCAATCTATAATGTCTCCAGTGTCTGGCCACCAAGCCACCCCTGCCAACGCTACCA
 AGCTGCAAGAATCTACTATATCATGGCAGAAGAAGTAGAGTGGACTATTGCCCTGACCGGAGCTGGGACGGG
 ATGGCACAACCAGTCTGAGAAGGACAGTTATGGTACATTCTCTGAGCAACAAGGATGGCTCTGGTTCAG
 ATACAAGAAAGCTGATTAGGGAAATACACTGATGGTACATTAGGATCCCTCGGCCAAGGACTGGACCAGAAGA
 AACTGGGAATCTGGGTCACCTATCAAAGGTGAAGTGGTGTATCTGACTGTTGATTCAAGAATAATGC
 CAGCCGCCCTACTCTGTGATGCTCATGGAGTGCTAGAATCTACTACTGCTGCGGCACTGGCTGAGCCCTGG
 TGAGGTGGTCACTTATCAGTGGAAACATCCCAGAGAGGTCTGGCCCTGGGCCAATGACTGCTGTTGTTCT
 GATCTATTATTCTGCACTGGTACATCCCAGAGACATGTATAAGTGGCTGGGCTGGGCCATTGGCTATCTGCCAAAA
 GGGCATCTGGAGGCCCATGGAGGACGGACTGACATGGGATTTGCAATTGTTGTTCTGATTGGCTATCTGCCAAAA
 AAATAAGCTTGGAGAGCAATAAAATGCAATCAATGGAAACTCTATGCCAACCTTGGGTCTTACAGGA
 TGAAACTTCTGGAGAGCAATAAAATGCAATCAATGGAAACTCTATGCCAACCTTGGGTCTTACACACCACCTCA
 GTACCAAGGAGAACGAGTGGCTGGTACATGCTGCCATGGGCAAGATGTTGATCTACACACCACCTCA
 TGCAGAGAGCTTCTCTATCGGAATGGCGAGAACTACGGGAGATGTGGTGGATGTTCCCAGGGACTTGA
 GGTTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCATGCTGG
 CATGGAGACCCCTTCACTGTTTCTGCAACAGAACACTTAAGCCCTCACCCTCATGCCAACAAAGAGACTGA
 AAAAGTGCCCTGGAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGAGTGCAGATCCCATAAAGAATGTGA
 GATGCTGGCCTCTGTTGGTGCATTAGTGTCACTTCTGCTGTTCTGGCTCTGGTGGAGTGGTTTG
 GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCTGGATGACAGCTTCAAGCTTCTGCT
 CAAACAGTAAACATCTGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTGCACCTCCAGCAGGCCATGGACT
 AGTCACTAACCCACACTCAAAGGGCATGGTGGAGAAGCAGAACAGGAGCAATCAAGCTTATCTGGATATTT
 CTTCTTATTATTTACATGGAAATAATGATTCACTTTCTTATGTTCTTGTCTACGTGGCACCT
 GGCACAAAGGGAGTACCTTATTATCCTACATGCCAAATTCAACAGCTACATTATTTCTGACACTGGGA
 AGGTATTGAAATTCTAGAAATGTATCCTCTCACAAAGTAGAGGACCAAGGAGAAAACCTATTGATTGGGTTCT
 ACTTCTTCAAGGACTCAGGAAATTCACTTGAACCTGAGGCAAGTGAAGCTGGTAAAGATAACCCACACTAAAC
 TAAAGCTAAGAATATGGCTGATGGAAATTGAAGGAGTGGCTGAGTATGGGAAATCCAATTGAATTGGATT
 CTCCTGGCAGTGAACACTTTGAAGAAGTGGTCAATGGGTTGTTGCTGCCATGAGCAGTGTACACCTCTGGAGC
 TAGAAGCTCCTCAGGAAAGCCAGTTCTCAAGTCTTAAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTC
 ATGTTTAGACAGCAAACCTATCCATTAAAGTACTTGTAGACCAAAAAAA

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FIGURE 234

MWAMESGHLLWALLFMQSLWPQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLSDIVASS
FLKSDKNRIGGTYKKTIYKEYKDDSYTDEVAQPAWLGFGLGPVLQAEVGDVILIHLKNFATRPy
TIHPHGVFYEKDSEGSLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTDADPACTLWiyH
SHVDAPRDIATGLIGPLITCKRGALDGNSPPQRQDVHDFFLFSVVDENLSWHLNENIATyC
SDPASVDKEDETFOESNRMHAINGFVFGNLPELNMCQAQKRVAWHLFGMGNEIDVHTAFFHGQM
LTTRGHHTDVANIFPATFVTAEMVPWEPTGLSCQVNSHFRDGMQALYKVKS CSMAPPV DLL
TGKVRQYFIEAHEIQWDYGPMDGHDSTGKNLREPGSISDKFFQKSSSRIGGTWKR VYEAFQD
ETFQEKMHLEEDRHLGILGPVIRAEVGDTIQVVFYNRASQPFSMQPHGVFYEKDYEGTVYNDG
SSYPGLVAKPFEKVTYRWTVPAPHAGPTAQDPACLTW MYFSAADPIRTNSTGLVGP LLVCRAGA
LGADGKQKGVDKEFFLIFTVLDENKSWSNQAAAMLDFRLLSEDIEGFQDSNRMHAINGFL
FSNLPRLDMCKGDTVAHLLGLGETDHGVMFQGNTVQLQGMRKGAAMLF PHTFVMAIMQPD
NLGTFE IYCQAGSHREAGMRAIYNVSQCPGHQATPRQRYQAARIYYIMAEEVEWDYCPDRSWE
REWHNQSEKDSYGYI FLSNKDGILLGSRYKAVFREYT DGT FRI PRPRTGPEEHLGILGPLIKG
EVGDILT VVFKNNASRPYSVHAHVLESTTVWPLAAEPGEVV TYQWNIPERSGPGP NDSACVS
WIYSAVDPIKDMYSGLVGPLAICQKGILEPHGGRSDMDREFALLFLIDENKS WYLEENVAT
HGSQDPGSINLQDET FLES NKMHAINGKLYANLRGLTMYQGERVAWYMLAMQDVD LHTIH FH
AESFLYRNGENYRADVVDLFP GTFEV VEMVASNP GTWLMCHVT DHV HAGMETLFTVFSRTEH
LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLL VVLA LGGVVWY
QHRQRKLRRNRRSILDDSFKLLSFKQ

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 1109-1130

N-glycosylation sites.amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,
876-880, 934-938**Glycosaminoglycan attachment site.**

amino acids 871-875

Tyrosine kinase phosphorylation sites.

amino acids 82-90, 137-145, 494-502, 513-521

N-myristoylation sites.amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,
843-849**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

Multicopper oxidases signature 2.

amino acids 1048-1060

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FIGURE 235

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTTAACACTACATTAGAAAAGCTTCATAG
CAAAACTGAGAGATTGAAGCAGTGATTATTTACATAGTTGTCATTAATATTGGAGCTCTGCTGTGCATAGA
GATGCCAACATACTTAGAATACACAGCTTCTGGGCCAGAAAATTGATCTCTGACTTTGAGCCTATCTGATTA
CTGCTGGTTCATCTTATTGTTAACTACTCTGCTAGGCTGAAAGGGAGAGACTCTCCCTGGTTGCAGAGCC
TGACTAGACAGGAATTCTGCAACTGCTCCAGCAGAACTATGGCACTGAGCTAGGTTAAATGCTGAGGAG**ATGG**
AAAACCTGTCACTGTCGATTGAGGATGTCAGGCAAGAAGTCCAGGAAGAAGCAGCTGGATGACTCTGGGGAGA
GAGATGAAAAATTATCCAAGTCAATCAGTTACCAAGTGAATTAATAGTCGGGTTTCAGAAACAGAGTCATTG
ATGGAATTATCATCAAAGGAGGATTAGGCAAAGAGGAGTCCCAAAATGAGAAACAGACAAAAAGAGTCTCTAC
CAACTTGGAAAAGAAGTTAACTAGAGTGCACATCAAAGTCACTGGACTTGAATAAAATGAATATCTTCTG
ACAAAAGCAGCATTGAGATTCTGTTGATGAAGAAAATGTTCTGAGAAAGATCTCATGGAAGACTTTTATCA
ACCGTATTTTATCATTCAGTGTGACAGAATGTTGAATTGCTCTTACAGTTCACTGCTTATGAGAAATTG
CCAGTCTAGAAATATAATAGATGAGTATCTACCCCTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA
TGACCTACACTATAGTCCTAATAGTCACCTACTGGAAAATGCACTGCTGCCACTGAAAAGCAGACACTGTATA
AAGAAAGTCGGGAAGCAGATTATTGGTAGATTCAAGAGTACTGACACATGATGCCCCATACATGATTACT
TCTATACCGTGAACAGATACTGTATCATCCGATCTCAGAACAGAAATGAGGCTAAAGAGTTCCACAGATTGA
AATACAGAAAACAGCATGGGCCTGTCAAATCTTAATTGAAAAGAATTCTGGAGTTTTGGAGGACTATT
TCAAACAGCTTGAATCAGATTGTTAATTGAGAAATCTGTATAAAATCAGGCCATTGAGAACCTGGAAAACCTA
CTGGCCTACGAAGGAGAAGGCGAACCTCAACCGAACAGCAGAAACAGTCTCTAAACTTCTCTCAGCATTCT
CTGGAGATGTGGCTTAGGTGCCAAAGGGATATTACAGGAAGAAAAGGAAATGAGAAAATATAACGTCACTC
TTATTGTGGAATGAGTATTGTTGTTATTGAGACTGTTCTGAGACTGTTCTGAGCTGTCAAAGA
TAGAACATGCTGTCAGTCCTTACCGTCTCGCCCTCCAAGAAGAGAAATCTTAAATTAGCCTCTGATATGG
TGTCAAGAGCAGAAACTATTCAAGAAGATAAAAGATCAGGCCATCGTTAAAGGGAGTGCTCCGAGACTCCATAG
TGATGCTGAACAGCTGAAGAGCTCACTCATTATGCTTCAAGAAAACGTTGATCTACTAAATAAGATAAGACTG
GCATGGCTGTTGAAAGCTAGTGAAGGACTAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGGA
AGAAAACCGAGAACATGAAGGATTGGCATAGAACATTCTATGTTTCTTATTGAGATTCTAATATGAA
CATTTCTTCAGAACATTATTGATAATTAGTTCTGCTGCCATTAAATCCATCTTCACTCTTATAGA
TATTTTAAGCTGTGAATTGAGTGGTATGGTCTATTCTACAGTGAAGTCTGATGCTTGTAGCACAGAACCCG
TACATGCAATTAGTCGCTTGTAACTGAGATAAGACCAAGAGGATAAACAGGACAATATAAGAACACCTC
TATGTCATTACTGATTAAAGGTTGTTCAAGGCATATAACATTCCAGGTTGTACTGTAAAGATTATA
ATGTCCTCATTTATTAGCATGCAAATTAAAGTCAAACATTGAAATTGCACTGTCATGTTGATGATGATTATCAGAA
AGGGCTCTGCCATGCTGATCTTATGAAAGAAATAGTTGTTTTCTTAAGGTAACATCAGAGGTGGGATT
ATCTGCCTCCTCACTAGAACACAGTCAGGAAAGAACATCCTCTGAGTTAAAACCAGAACAGGTTA
TGTTAAATCTGGCATTAGTGACAGATCAAATGCATACTTGAACATAAGATTGGCTCAGCTAGCAGTCTTC
ATGGTGAAGTGAACACATCTGGTTGAAAATAATTGTTGCTTCACTGTAACCATGTTGCTCTTCTTATGT
ATGTGTTGACTTGTAAATTGGTAAGTTATAAGCCAGACATAGATTGCTCTTAAATAAAACTTCAGGGG
CACGTATGTCCTCAGTACAAGTGACTGACTATCAAGTTAACACTCAGATGCAAGCTTGGCTCTTCATAAAAG
TTTTTATGCATATGTCCTCATAAGTGGCTCAATTAAAGAACATTGTAACATGTTAAACTGACTTAAATCAGATAT
TTTTCAAGAGTTAGGGAAAGTTGAAGTGTGTTACTGTTGCTCTTGAGGCCCTTCTGGGGAAAAAAATACA
TATCCATCTATCTATCTATATAAAACTGTTGATACATTCTACTGTTGAACAACTATTGCTTAAATTAAATG
TTTCATTCTCCAGAGTCCCCAAAGCCACATGGCATTATTATAGTCATTGAGATGCCTGTAGAGAACATGAA
AGTATGACTCCGTTAGAGGGAAATGGGTTCTGGGTGAATTCCAACGAAGCATACCTAGGGTAACAGTGA
ACCTACCTGGGTTGTTGGTAAAGGATTATGAGTGTCTGGCTGTAAGCAAGAACATGAGTGGATTATAA
ACTTGAAGATTCTCTGTTAAAGTCACAAAATGATGACAAACAAATTGTTGAGATGTTATTAAACGTTG
ATTTTATAACATACTCAAGGAAGAGTATGAGTAAGTGTCTTATAAAATTAGACTAAATTCTGATGGATGCA
GAATTCAATTAAATAAAATTGAGCCTGTTACGTAATTGAATATTAAATAAAATTGAAAATTCAAA

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FIGURE 236

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKSISFTSESESISRVSETESFDGNSSKGGLGKE
ESQNEKQTKKSLLPTEKKLTRVPSKSDLNKNYEYLSLDKSSTSVDENVPEKDLHGRLFI
NRIFHISADRMFELLFTSSRFMQKFASSRNIIDVVSTPWTAELGGDQLRTMTYTIVLNSPLTG
KCTAATEKQTLYKESREARFYLVDSEVLTHDVPLYHDYFYTVNRYCIIRSSKQKCRLRVSTDLK
YRKQPWGLVKSLIEKNSSLEDYFKQLES DLLIEESVLNQAIEDPGKLTGLRRRRRTFNRTA
ETVPKLSSQHSSGDVGLGAKGDTGKKEMENYNVTLIVVMSIFVLLLVLLNVTLFLKLSKIE
HAAQSFYRLRLQEEKSILNLASDMVSRAETIQKNKDQAHRLKGVLRDSIVMLEQLKSSLIMLQK
TFDLLNKNTGMAVES

Transmembrane domain:

amino acids 352-371

N-glycosylation sites.

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 81-85, 307-311

Tyrosine kinase phosphorylation sites.

amino acids 202-211, 246-254, 341-349

N-myristoylation site.

amino acids 259-265

Amidation site.

amino acids 339-343

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FIGURE 237

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCTGCTCGCGCAATCCTGACCTGCT
CTGGCGCCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTCAATGCTGAAAAGTTCTC
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGCTTCCTGGCAAGAAGGACCA
CCTGTCCATGTCCACCAGGCCATCAGGCCACAGAGGAGGGCGGCCTCACGTCCACATGGA
GTTCCCGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGCTCCGAGGG
ACACTTCAGAGTCCCAGGCTTACCTGACGTGCGCATCGTGGACACAGACTACAGCTC
CTTCGCCGTCTTACATCTACAAGGAGCTGGAGGGGCCCTCAGCACCATGGTGCAGCTCTA
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTCCAGGACTTCTACCCGACCC
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCAGTCAGATGCATGCAACCCTGAGAGCAA
GGAGGCGCCTGAACACTCCGGAGCCCCACCCCCGCCCTCCAGGTGGAGCCAAGCAGCAG
GCGCCTTGCCCCCTGGAGTCAAGACCCACAGCCCTGGGGACCACCTGGAGTCTCTCCATCCT
CCACCCCCCGCCTGTGGATGCCTTGTGGACGTCTTTCTATTCAATAAACAGATGCTGCA
GCCTCA

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FIGURE 238

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMASDCRVFLGKKDHLSMSTRAI
RPTEEGGLHVHMEFPAGCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDTSFAVLYIYK
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

Signal peptide:

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 110-117

N-myristoylation sites.

amino acids 7-13, 79-85, 130-136

Amidation site.

amino acids 50-54

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FIGURE 239

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCGAGGCGGTCA
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCCTGGATATGGAGCTGGCTGCT
GCCAAGTCCGGGGCCCGCGCCGCTGCCTAGCGCGTCTGGGACTCTGTGGGACGCGCCCCG
CGCCCGGGCTCGGGGACCCGTAGAGCCCAGCGCTCGCGCA**T**GCCCTGCTCTCGCGCCCCG
GCTCACCCCTCTGCTCCTCATGGCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACAC
CGACTGGAGAGCCACCCCTGAAGACCATCCGAACGGCGTTCATAGATAAGATAGACACGTACCTGAA
CGCCGCCTTGGACCTCCTGGAGGCAGGACGGTCTGCCAGTATAATGCAGTGACGGATC
TAAGCCTTCCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT
TGGTGTTCATCTAACATTGGTATCCCTCCCTGACAAAGTGTGCAACCAACACGACAGGTG
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCAA
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTAGGCATGTGAAACAAAC
AGTGGAGCTTGTGTTGACAGTGTATACATTAGGTTGAAACCATACTGGACAGCCAACG
AGCCGCATGCAGGTGTCAATTGAAGAAAAACTGATCTTTAAAGGAGATGCCGACAGCTAGT
GACAGATGAAGATGGAAGAACATAACCTTGACAAATAACTAATGTTTACAACATAAAACT
GTCTTATTTGTGAAAGGATTATTTGAGACCTTAAATAATTATCTTGATGTTAAAC
CTCAAAGCAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTGTCTCAGGTATCTT
CCCCAGCATTGCTCCCTACTTAGTATGCCAAATGTCTGACCAATATCAAAACAAGTGCTT
GTTAGCGGAGAATTTGAAAAGAGGAATATAACTCAATTTCACAACCACATTACCAAA
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG
GGAAATTATCACTTACAAGTATTGTTACTATGAAATTAAATACACATTATGCCTAGAA
GGAACGGACTTTTTCTATTAAATTACACATAATATGTAATTAAAGTACAACATAATAT
GTTGTTCTGTAGCCGTTGAGCATATGAGTAAGTCACATTCTATTAGGACTACTAACAA
GGACAAGGTTCCATTTCAGTTGAAACCATCAGCTGATAACCTCGTAGGGAG
CAACCCAGGATAGCTAAGTGTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTAGAA
GCATAGCCACTCCCATTGAGCTACTCACATGACAAATGTCATTTGCTATAACCTT
GCCAAGTTAGAGAAAAGATGGATTAATGAGATAATGAAAAGATATTAAACCTAAAAAAA
AAAAAAAAAAAAAAA

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FIGURE 240

MALLSRPALTLLLLLMAAVVRCQEQAQTTDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC
QYKCSDGSKPFPRYGYKPSPPNGCGSPLFGVHLNIGIPSLTKCCNQHDRCYETCGKSKNDCDE
EFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACRCHYEEKTDL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites:

amino acids 57-63, 93-99

Phospholipase A2 histidine active site:

amino acids 106-114

Neuraxin and MAP1B proteins repeat proteins Block:

amino acids 109-137

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FIGURE 241

GATTCCGAGCGCCTCCACTGCTGGTCCGTGGCCAGATCAACTGCCGCCTGGGCCGGCGTT
CCCTGAGAGTCTGAGCGCTGCCGCACCCCTCCGAGCTTCTATTGCCGTAGCAGACGTCC
GTCTGCCGCTATCTCCGCCAATACGGAAGCGGCCTAGTCCTCCGGCTCGACAGCTGGGTG
TCCAGGCCATGGGCAGCCCTGGCGCTGGGAGCACGGACGGGGCGCCGCGCAGCTGCCCTC
TCGTGCTCACCGCCTGGGCCGCGGTGGGAGCTGGGAGCTGGCTTACGTGCTGGTGCTCG
GTCCCCGGGCCGCCGCGCTGGGACCCCTGGCCCGGGCTTGCAGCTGGCGCTGGCCGCTTCC
AGCTGCTAACCTGCTGGCAACGTGGGCTCTTCCTGCCTCGGATCCCAGCATCCGTGGCG
TGATGCTGGCCGGCGCGGTCTGGGCCAGGGCTGGGCTACTGCTACCAATGCCAAAGCCAGG
TGCCGCCACGCAGCGGACACTGCTCTGCCCGCTGCATCCTCGCTCGGACCACCACT
GCCGCCTGCTGGGCCGCTGCGTGGCTTCGGCAACTACCGGCCCTCCTGTGCCTGCTGCTTC
ATGCCGCCGGCGCTGCTCCACGTCTGTGCTGGCCCTGCACGTGCGTGGGCCCTGCTGC
GAGCCCACACGCCCTCCACATGGCTGCCCTCCTGCTCCCTGGCTATGTTGCTCACAG
GCAGAGTGTCTCTGGCACAGTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGC
TGCTGTGCGGGCTGGGCTGCTCTCCATGGATGCTGCTGCGTGGGCCAGACCAATGG
AGTGGCTGGGCCAGCACTCCTATGACCTGGTCCCTGCCACAACCTGCAGGCAGCCCTGG
GGCCCGCTGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGATGG
TCACCTCCAGACCACAGCAGATGTGGACACACAGCCTCCTGACTCCAGGAAGAGCCAGAGC
TGTGCAGGGAGGAAGGGGTGAGAGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT
GGACCTAACATCTGCATTGGACAACCTCCACCCCTTCCTGGCCTGCCCTGCCCTACA
CTCCTACGTGTCCAGGGCTGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG
GGGCTGCTCAGGCCGCCTAGCTGCCCTTGCCAGGTTAATAAGCACTGACTTGTAA

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FIGURE 242

MGQPWAAGSTDGAPAQLPLVLTALWAAAVGLELAYVLVLGPAGPPPLGPLARALQLALAAFQLL
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCRL
LGRCVGFNYRPFLCLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLPWLMLLTGRV
SLAQFALAFVTDTCVAGALLCGAGLLFHGMLLRGQTWEARGQHSYDLGPCHNLQAALGPR
WALVWLWPFLASPLPGDGITFQTTADVGHTAS

Important features:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 51-66, 143-160, 174-191, 198-214

N-myristoylation sites:

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

Leucine zipper pattern:

amino acids 143-165, 150-172, 157-179, 164-186

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FIGURE 243

CTTGTCTTGTCGGTTGTGATTTCTAATCTCTGATTTCTCTCGGACGCTCTC
CCTCTTCGGACCCATTCTCCCCTGCTTCATGCCCTGATAGCCTGGCCCTTCCGGCTTCC
TTCGCTACCAGGGACGCCCTAGTTCTGAATTCTGGCTGGCTCCACCCTCCGCCTCAT
CTTCCTCAAGAGTCGCCCTCTGGGGCTCCTGTGTAATCGTCGCCTCTGGGTATTT
CTGTGAACCTCGTCTCACACCATCCGCCATCTCTGCCTGGCCCTTTCTGTACAG
CCAGCTCTGTGCTCTTCTCCCCCTCTAAAGACTCCTCTCCCTGAGAGCCCCA
CCTTGTGCCCACTCCTCATTTCTACGCCTCCCTCTGTGCTGGCCTCTCTCCCTG
CAAGGTTCCATTCCATCAATTGTTGTCTTGAGGGTGGCATCCCTCTGACTACTGCT
CCATCCTTTTTTTTTTTTTGCTGAGGATTCACTCAATCTTCTGGT
TGCGTCTCCACTGTACTCAGCTTGTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC
GTGTGCTGTCTCTGATTGGCCTAATCTCCCTCACCCCCGTGAGATCTGTTGTCAGCCTC
GTTCTCTTCCGTGTCAGCTTCTGCGGGCTTCTGGCACCTTCTGGCACAGATTTC
TGGGTTACAGAGCATGTGTCAGGCATTGCAGGCAGAAAAGGGTGGCGACGTGACCTCT
AGCTGGACTGCTGGGAGGGAGCTGTCCTAGATAAAATTGAAAGAACAGTGACCCAGAGA
CAGGTGGACAAGAATTGGGACTGATGGAACTGAGCTGGATCCAGACTGAAACTGATT
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGCCTGGGACCCAGCATTGAGACT
TGTGCAGCTGTTCTGCCTCTAGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTTTGTG
CTATGAAGCAACAGCCTCAAGATTAGCAGCTGTTGCTTCCATACTGGAAGTGGCTCTGAT
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCAGGAGACGCTAGTGTTCATTGAGACAGG
GACTGCAAGGGAGTTGGCTTAAAGGCTGCAGCTCGTCTCGTCTTACCCCTGCGCAAAT
CTCCTACCTGTTCCCCACCCGGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA
TCTCTGCAACAACCTCACCAATTGGAGCCTTGTGAAACTCAAGGCCAGCACTCTAACGTC
TATCACATCTGCGTCTGTAGCTGCCGACCTGTGAGGAGACATGAAGGATTGCCTCCC
AAATTGTCAACCAATTCTGCCCCTGGCTGTTCTACGTGTTACAGTCCACCTTAA
ATTCAGGCAGGGTTCTCAATACCACCTCCTCATGGGAGCATCAAAGTGAAGTGGCTCGTGAACATAACCA
GCTTTAGCAGATTTCATCATATTGGGAGCATCAAAGTGAAGTGGCTCGTCAACATCTTAGA
GAAGTCTCAGATTGTTGGTGCAGCATCTCCAGGCAAGATCTGCTGGGTGTCGTCTTAGG
CCTCCTGTTGCCTCAGGGACTTGACCATCTAGCTGCACCCAGACACTCTTCA
CATAACAAATAAAAGCAGAGTCCCTAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 244

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM
GCAREHNQLLADFHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFARFD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites:

amino acids 117-121, 183-187

N-myristoylation sites:

amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,
235-241, 239-245

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 181-192

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FIGURE 245

GTGGAGTTGGTGGTGTGGGAGCCTCCCTGAGGGGCACCGCGTCTCAGGAGCTGGCCTCAGTCGGCG
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGCGTGGCGCTGGCGCTGCGGGCCTGACCGG
TCCGCTCATGGTGCCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTCTCACCTCCTTTAG
ACTGAGATCTGCCAAGTTTCCGGCATTGCTCTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT
GTGTGTATTGTCATGAACCGAATGAATTCCCAGAACAGTGGTTCACTCAGCGCAGGCGAATGGCTCTGGGAT
TGTTATTCTCTGCTTGTGATGTGATATGGGTGCTTCCTCTGAACCTACTTCGTATGTTTACCCAGTACAA
CAAACCATTCTCAGCACCTTGCAAAAACATCTATGTTGTTGACCTTTGGCCTTATTATTTGGAAGCC
ATGGAGACAACAGTGTACAAGAGGACTCGCGGAAAGCATGCTGCTTTTGAGATGCTGAAGGTTACTTG
TGCTTGACAACAGATACAACTATGAATAGTTCTTGAGTGAACCTCTGTATGTGCCTGTGAAATTCCATGATCT
TCCAAGTAAAAACCTGAGAGCACAAACATTGATACTGAAAAACCCCCAAAAAGTCGTGTGAGGTTCAGTA
TATCATGGAGATTGACAGCCTCCGTCAAGTCATGCATTGGAGCAGAAAGTGTCTCGATGTCAATATCCTGTGAA
AGAACAGAACATCCATACTGAAAACTGTGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTG
CTTGTGTTGGTTTGCAAAATTGTCAAGAACGACTTCAGACACACAAGTGTCTAGTTAATATTT
ATCTTCAACTCCGGACTTTTACCTTAATCCTGCTGAGTATTCCAGTAAACAGTGGAGATAGATTACCC
TTCTAAACTATTAGCTGTAATTAAAGCATTGGAGGCGTTGACTGGTAAACCTGGCAGGGCTGAAAAACCTGC
TGGAAGAGACACAGTAGGTTCCATTGGTCTTGTGAGGCCATGCTCTATGCTGTCTATATTGTTATGATTAA
GAGAAAAGTAGATAGAGAACAGAACAGTGGATATTCCAAGTCTTGGTTGAGGTTGTTAATCTGCTGCT
CTTATGCCAGGTTCTTTACTCATTATAACTGGATTGAGGACTTCAGAGTTCCAAATAAGTGTATTAA
GTGCATTATCATTAAATGGCCTTATTGGAACAGTACTCTCAGAGTTCTGTGGTTGTGGGCTGCTTCTTACCTC
ATCATTGATAGCACACTGCATAAGCCTTACAATACCTCTGCCATAATAGCTGACATGTGTATGCAAAGGT
GCAGTTTCTTGGTTATTGGTCAGGAGCTATCCCTGTATTGTTTACATTGTAACCTCCTATGCCA
TTATAATAATTGGATCCTGTGATGGGGAATCAAGAACATTTGCTTTATATGCAGAAAACATCGAATTCA
GAGAGTCCAGAACAGCGAACAGTGTGAGAGTCTCATTCTATGCACAGTGTGTTCTCAGGAGGATGGAGCTAG
TTAGCTGTCTGTTGCTGTAGCCCAGCTGATAATGAACTATACAGCGAACAGAACATCTGGCAAGTTTG
TAGAAAAATGTTCAAGTGCCTAGTGTGAAACTTAAACAGTTGAGTCTTGTAAACTCTAAATATTTCTC
ATACCTGTTTCTTCATAATGAAGCACTTGCTATGTAGCTGTACATATCACTACAGTTAGGAAG
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTACACATCTCAAGGAATTCAAGCTGTTGAAATCATTG
ACTAATCAAGGAATAAACTTAATGTTGGACTTATTTCACATGTTAAATGCTGGAATATATTGAAAT
GTTTCAAGAAACTTAAGTGTCATAGACCAGTATTCTGACAGGTAAAATGCTAAAGTACCTGTAA
TAAGTGTGGATTATTTGGTTTGAGAATATTGCAAATTAACCACACAAAAATGTTAATTATGCAAC
AAGCATGTTGTGCAAAATTTCATGGGACTTAAAAGAACATAAGTATTGAGAAAATATCTGGTTCACTTACACTA
CATTTACTGTATTATTCTTATAGCATTAGGTGCCTGTATTAAATCTGTGACAAACCATGGCAAATT
AAGGGGAAGTATTATTATAAAATGAAGAACATATGTATTCTAAAGGCTATATTGCTGTAACCTTAATTGATAAAG
CTCTGTTAATTAGAGTTGAAGAAATAGTCTCCCTCAATTAGAAATTTCATAATGGAATGATTAAATT
GAAGTGACAAAGAGTATTATTAAATACAATGTTATAAAAAAA

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FIGURE 246

MVPPRRHRGAGRPGVLSSSPPFRLRSAKFGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF
TQRRRMALGIVILLVDVIWVASSELTSYVFTQYNKPFFSTFAKTSMFVLYLLGFIIWKPWRQ
QCTRGLRGKHAAFFADAEGYFAACTDDTMNSSLSEPLYVPVKFHDLPEKPESTNIDTEKTP
KKSVRVFSNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN
LAGSEKPAGRDTVGSIWSLAGAMLYAVYIVMIKRKVDRDKLDIPMFFGVGLFNLLLLWPGF
FLLHYTGfedfefPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALS廖IPLSIIA
DMCMQKVQFSWLFFAGAI PVFFSFFIVTLLCHYNNWDPMVMVGIRRIFAFICRKHRIQRVPEDS
EQCESLISMHSVSQEDGAS

Important features:**Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,
364-379, 399-419, 453-472

N-glycosylation sites:

amino acids 157-161, 255-259

N-myristoylation sites:

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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FIGURE 247

CGTCTGTAGAGATATCATGAACCTCAACTTAGCTTGGTACTTCCTCCCTGAAGACAGAGGG
CAGAACTCTGAGTTCCAGAACCACTTCAACTGTATTGGGGACCAATCACTGACTCTATTCT
TGTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTCTAAAAGTGAA
TCCTGCTACTAAAATAATTCAAGATGATATTTTCCAATTCTACAATCTGCTTGTTTAT
TTAGTTGTTCTCTCTTCCCAGTTCCAGAGACTGGAGCTAAACTGGGCTTCAACA
TCATCATGAAGTTATCCTCCTGGGCCCTTGAATCTGACTGTTGCTTGGCCTTAATC
CAGATTACACAGTCAGCTCCACTCCCCCTACTTGGTCTATTGAAATCTGACTACTGCCCT
GCGCTGGAGTCCTGATCCACCCGCTTGGGTGATCACAGCTGCACACTGCAATTACCAAAGC
TTCGGGTGATATTGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG
GCTATGAGAAGATGATTCATCATCCACACTCTCAGTCACCTCTATTGATCATGACATCATGC
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTGCCAACCTGCCCTACC
AAACTATCTGAAAATACCATGTGCTCTGCTCTACCTGGAGCTACAATGTGTGATATCT
ACAAAGAGCCGATTCACTGCAAACACTGTGAACATCTCTGTAATCTCAAGCCTCAGTGTGCG
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGGCATTGTGCCAGGAAGGA
GGCAGCCCTGCAAGGAAGTTCTGCTGCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC
TGTCTTTCGGATGGATGTGTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTACT
ATATACCCCTGGATTGAAAATGTAATCCAAAATAACTTGAGCTGTGGCAGTTGTGGACCATATGA
CACAGCTTGTCCCCATCGTCACCTTAGAATTAAATATAACTCCCTC

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FIGURE 248

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYIHKSDYLPAGVLIHPLWVITAAHCNLPKLR
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKTEAELNDYVKLANLPYQT
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ
PCKEVSAAPAIICNGMLQGILSFADGCVLRADVGIYAKIFYYIPWIENVIQNN

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation sites:

amino acids 11-15, 156-160, 173-177

Tyrosine kinase phosphorylation site:

amino acids 108-117

N-myristoylation sites:

amino acids 182-188, 203-209

Amidation site:

amino acids 185-189

Serine proteases, trypsin family, histidine active site:

amino acids 52-58

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FIGURE 249

GCGAGGCGGCCGCTGTCTCTGCTGGCTTCCCGACCAAGTACTGCTGCGACGACCCGC
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC
TGTCCGTAGCAGCAGTGGTTCTTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGCAGAAGTGCAAAGTGA
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG
TGAACCTCAAACGCCTCCTCCATCATTGCTTCATGCCACAGTGACCACAGTGACATTCCAG
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA
ATAAAATGTCTCCATACCATCAA

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FIGURE 250

MWWLSIGALIGLSVAAVVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV
NTGMAAEVPKVSPLQQSYSCLNPQLESNEGQAVNSKRLLHHCFMATVTTSDIPGSPEEASVPN
PDLCGPVP

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 7-13, 11-17, 62-68, 93-99

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FIGURE 251

GTGGTTGGATTGAGCCGGCCCGGCCGGCGCCAGTCGGAGGGGTGGCAGTGAGCGGCG
GCAGAGGCTACGGGCTCGGTTGGCTGACTGGGAGTCGGCAGGCAGGAACC**ATGCGAG**
GCCAGCGAGCCTGCTGGGCCCGCCCTGCCTCCGCCTCCTCTGCTGCTGGGTT
ACAGGCAGCCGCTGTCCACCTCTACTCCGGGTCTAGTACAGCGCTGGCGTACGGCAAGGTCT
GCCTCGCTCCCTGCTACAACCTTGGGGCAGTGACACCGCTGTTGATGCTGCCTTG
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTGGAGTGGTGTGTCCTGG
TGATCGTGTGACAGGCTCATTGTAGCTATGCCAACCTGTGTGTCCTGCCTCATCCTCC
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA
TTGTTCCACTACTACCAGGCCATCACCACTCCGCCTGGTACCCACCCAGGGCAGGAATG
ATATGCCACCGTCTCCATCTGTAAGAAGTGCATTACCCAAAGCCAGCCCACACACCACT
GCAGCATCTGCAACAGGTGTGCTGAAGATGGATACCCTGCCCCGGCTAAACAATTGTG
TGGGCCACTATAACCATCGGTACTTCTCTTCTGCTTTCATGACTCTGGCTGTGTCT
ACTGCAGCTATGGAAGTTGGACCTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC
AGACCCACCAACCCACCTCTCCTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT
GGTTCTGTGCAGTTGTGGCACTTGCCCTGGTGCCTAACTGTATGGCATGCTGTTCTCA
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTGGCTACAGG
CCAAGGGCAGAGTATTAGGAATCCTTACAACACTACGGCTGCTGGACAACGTGGAAAGGTATTCC
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGTCTTACCTCTAGTCACCTGCC
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTGTGATGG
CAGTG**TGAG**CTGGACTGTGTCAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTCA
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTACCACTGCAGAAGAAAGACACAATGT
GGAGAAATCTTAGGACTGACATCCCTTACTCAGGCAAACAGAAGTTCCAACCCAGACTAGG
GGTCAGGCAGCTAGCTACCTACCTTGCCTGGAGTCGCTGACCCGGACCTCCAGGATACAGCAC
TGGAGTTGCCACCAACCTCTACTTGCTGTGAAAAAAACACCTGACTAGTACAGCTGAGA
TCTGGCTCTCAACAGGGCAAAGATAACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA
TGCTGCTTAAGGGAGCACAAATAAGGTATTGATTTAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 252

MRGQRSLLLGPARNCLRLLLLGYRRRCPPLLRGVLQRWRYGKVCLRSLLYNSFGGSDTAVDA
AFEPVYWLVDNVIRWFGVVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL
ILIVFHYYQAITTGGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHC PWLN
NCVGHYNHRYFFSFCFFMTLGCVYCSYGSWDLFREAYAAIETYHQTPPPFSFRERMTHKSLV
YLWFLCSSVALALGALTWHAVLISRGETSIERHINKERRRLQAKGRVFRNPYNYGCLDNWK
VFLGVDTGRHWLTRVLLPSSHLPNGNGMSWEPPPWTVAHSASVMAV

Important features:**Transmembrane domain:**

amino acids 88-100, 202-216, 254-274

N-myristylation sites:

amino acids 55-61, 56-62, 92-98, 210-216, 309-315, 319-325, 340-346

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 201-212

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FIGURE 253

TGCAAGCGCCTTCCCTTCCTCTCCCTACTGGCCTTGCCTAAGCCAAGACCTGGCATCGCCTGGC
TGCAGGGGCTGCCAGGCCAGCTGACTTTCAGGTATGGGGAGGGCAGGCACCATGAAGCCAGTGTGGGTC
GCCACCCCTCTGTGGATGCTACTGCTGGTCCCAGGTGGGGCCGGAAAGGGTCCCCAGAACAGGCCCTCC
TTCTACTATGGAACCTCCCTCTGGCTTCTGGCTGGCAGTCTGCCTACAGACGGAGGGCCTGG
GACCAGGACGGAAAGGGCTAGCATCTGGACGTCTCACACACAGTGGGAAGGGAAAGTGCTTGGAAATGAG
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAACTGCACGTCAAC
CACTACCGATTCTCCCTGTCTGGCCCCGGCTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA
ATCGAATTCTACAGTGATCTTATCGATGCCCTCTGAGCAGCAACATCACTCCATCGTACGCTTGCACCACACTGG
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGCCAACTACTTCAGAGACTAC
GCCAACCTGTGCTTGAGGCCTTGGGACCGTGTGAAGCACTGGATCACGTTAGTGAACCTCGGGCAATGGCA
GAAAAAGGCTATGAGACGGCCACCATGCGCCGGCCGTGAAGCTCCGGCACCGGCTGTACAAGGCAGCACAC
CACATCATTAAGGCCACGCCAAACCTGGCATTCTATAACACCACGTGGCGAGCAAGCAGCAAGGTCTGGT
GGAATTTCACTGAACCTGTGACTGGGGGAAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCAGAGA
TACCTACAGTTCTGCTGGCTGGTTGCCAACCCATTATGCCGGTACTACCCCAAGTCATGAAGGACTAC
ATTGGAAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTCAGGTTACGGTGTCACTCCAGGAGAACAGCTAC
ATTAAAGGCACATCCGATTCTGGATTAGGTCACTTACTACTCGGTACATCACGGAAAGGAACCTACCCCTCC
CGCCAGGGGCCAGTACCAAGAACGATCGTACTTGATAGAGCTGGTGCACCAAAGTGGCCAGATCTGGGTCT
AAATGGCTATATTCTGTGCCATGGGATTAGGAGGCTCTTAACCTTGCTCAGACTCAATACGGTGTACCTCC
ATATATGTGATGGAAAATGGAGCATCTCAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAACATTCAATAC
CTTAAAGGATACATAAAATGAAATGCTAAAGCTATAAAAGATGGTCTAATATAAAGGGTATACTTCCCTGGTCT
CTGTTGGATAAGTTGAATGGAGAAAGGACTTCAGATAGATGGATTCTACTATGTTGAATTAAACGACAGA
AATAAGCCTCGCTATCCAAAGGCTCAGTCAATATTACAAGAACGATTATCATTGCCAATGGGTTCCCAATCCA
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTGGAAACTTGCTCTATCAACAATCAGATGCTTGCAGAGCCT
TTGCTAAGTCACATGCAAATGGTACGGAGATCGTGGTACCCACTGTCTGCCCTCTGTGTCCTCATCACTGCT
GTTCTACTAATGCTCCTCCGTGAGGAGGCAGAGCTGAGACAGGATTATCAATTGGAGCTTCAAAAGAACATT
CAGGATCTCCCTCCCTTCTGCTTGAGGGTTCCACATTGCTGTTCAAGGTTCTACAATAATTACCTTT
TTTCTCTTCTCTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAGCAGAAATTAA

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FIGURE 254

MKPVWVATLLWMLLVPRLGAARKGSPEEASFYYGTFPLGFSGVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG
KVLGNETADVCADGYYKVQEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSIDLIDALLSSNITPI
VTLHHWDLQPOLLQVKYGGWQNVS MANYFRDYANLCFEAFGDRVKHITFSDPRAMAEKGYETGHAPGLKLRTG
LYKAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCDWGE PVDISNPKDLEAAERYLQFCLGWFANPIYAGDYP
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKS YIKGTSDLGLGHFTTRYITERNYP SRQGPSYQNDRDLIELVDPN
WPDLGSKWLYSVPWGFRRLINFAQTQYGDPIYVMENGASQKFHCTQLCDEWRRIQYLKYINEMLKAIKDGANIK
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDRNKP RYPKASVQYYKKIIIANGFPNPREVESWYLKALETCSINNQ
MLAAEPLLSHMQMVTEIVVPTVCSLCVLITAVLLMLLRRQS

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 541-558

N-glycosylation sites:

amino acids 80-84, 171-175, 245-249

Glycosaminoglycan attachment site:

amino acids 72-76

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27, 564-568

Tyrosine kinase phosphorylation sites:

amino acids 203-211, 347-355, 460-468, 507-514

N-myristoylation sites:

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

Amidation site:

amino acids 307-311

Glycosyl hydrolases family 1 active site:

amino acids 407-416

Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

Motif name Glycosyl hydrolases family:

amino acids 37- 67

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FIGURE 255

CGCGAAGATGGAAAGGTGGTTTGATCACCGGGCTAGCAGTGCATTGGCTGCCCTCTG
CAAGCGGCTGCTGGCGGAAGATGATGAGCTCATCTGTGTTGGCGTGCAGGAACATGAGCAA
GGCAGAAGCTGTCTGTGCTGCTGCTGGCCTCTCACCCCAGTGCTGAGGTACCCATTGTCCA
GGTGGATGTCAGCAACCTGCAGTCGGTCTCCGGGCCTCAAGGAACCTAACGAAAGGTTCA
GAGATTAGACTGTATATCTAAATGCTGGGATCATGCCTAAATCCACAACAAATATCAAAGC
ACTTTCTTGGCCTCTTCAAGAAAAGTGATTCATATGTTCTCCACAGCTGAAGGCCTGCT
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTGAGACCAATGTCTTGG
CCATTTATCCTGATTGGAACTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTCAAGCCTCGAGGACTCCAGCACAG
CAAAGGCAAGGAACCCTACAGCTCTCCAAATATGCCACTGACCTTGAGTGAGCTGGCTTGAA
CAGGAACCTCAACCAGCAGGGTCTCTATTCAAATGTGGCCTGTCCAGGTACAGCATTGACCAA
TTTGACATATGGAATTCTGCCTCCGTTATATGGACGCTGTTGATGCCGGCAATTGCTACT
TCGCTTTTGCAAATGCATTCACTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT
TTTCCACCAAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCT
TGGAAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTAA
TCAAAAGTTACTGGAACTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC
CAGGCTCAGTGGCTCATGCCTATAATTCCAGCAGTGGGAGGCCAAGGCAGAAGGATCACTT
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTGTCTCTACAAAAAGAAAT
AAAAATAATAGCTGGGTGTGGTGGCATGCCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG
GGAGGATCTTGGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC
AGCCTGGGTGACAGCGAGACCCCTGTCTCAAAATATGTATATATTAAATATATATAAAACCA
GAGCTGACAATGACACTCTGGAACATTGCATACCTCTGTACATTCTGGGTACATGGATTTC
TACTGAGTTGGATAATATGCATTGTAATAAACTATGAACTATGAA

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FIGURE 256

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD
VSNLQSVFRASKELQRFQRLDCIYLNAGIMPQPNLNIKALFFGLFSRKVIHMFSTAEGLLTQ
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSRSARKSNFSLEDFQHSKG
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLRF
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAEKFYQK
LLELEKHIRVTIQKTDNQARLSGSCL

Important features:**Transmembrane domain:**

amino acids 234-254

N-glycosylation sites:

amino acids 37-41, 178-182, 229-233, 263-267

Glycosaminoglycan attachment site:

amino acids 12-16

N-myristoylation sites:

amino acids 9-15, 13-19, 15-21, 215-221, 224-230

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FIGURE 257

CGGACGCGTGGGCCGTATGCGCGCTCTGTGGAGTGCACCTGGGTTGGGGCACTGTGCC
CCAGCCCCCTGCTCCTTGGACTCTACTTCTGTTGCAGCCCCATTGGCCTGCTGGGGAGA
AGACCCGCCAGGTGTCTCTGGAGGTCACTCCCTAACACTGGCTGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCCCTGAGCATCAACTGGAGCCTCCTGC
TATCCCCTGAGCCCAGTGGGCCTGATGGTGCTCCCTAACGGACAGCATTCAAGTGGTTCTTCTG
CCCTGTTTACCAAGGCTGTTGAGTTGACAGCACCAACGTGTCCGATAACGGCAGCAAAGC
CTTTGGGAAGACCATACTCCATACTCCTGGCCGATTCTCTTGGAACAAACATCACTGATT
CATTGGATCCTGCCACCCCTGAGTGCCACATTCAAGGCCACCCATGAACGACCCTACCAGGA
CTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTCCAGGTCCAGCCGACCAGCCC
AACCCCCCTGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGAAACCGTTCCCTGTTGGCTGGAGGTAGCCACATTGGCCAGGGCCCTGACT
GCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTCCAGTTGG
ACCAGCTACTGTGGGCTCCCTCCATCAGGCTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCCGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCTCTCATCCTGCCTTAG
CATACTCTTCCCCAGTCACCCATTGTCCGAGCCTTGGTCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGCTTCCCTCCAGGTCTGCTAGGGCTCATGCTGCTAGGGGGCGGCTGGTTCTGCTGC
TCATGGCAGTGGCCCTGGGTGCCCTGGGCTCATGCTGCTAGGGGGCGGCTGGTTCTGCTGC
TGCACCACAAGAAGTACTCAGAGTACCAAGTCCATAAAATTAAAGGCCGCTCTGGAGGGAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGGCATCAAGTCCAGCC
GGCCCTTCACTCCCCATCTGCTTCTGTGGAACCTCAGAGGCCAGCCTGACTTCC
AGACCCCCAGGTGGGCTTCCCTCATACTTGTGGGGACTTGGAGGCAGGGACAG
GGCTATTGATAAGGTCCCCCTGGTGTGCCTTGCATCTCCACACATTCCCTGGATGG
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTACAGGGAAAAAAA

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FIGURE 258

MRGSVECTWGWHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIRAVG
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLSPEPDGGLMVLPKDSIQFSSALVFTR
LLEFDSTNVSDTAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHPMNDPTRTFANGS
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE
QHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIMAVAL
GAPGLMLLGGGLVLLHHKKYSEYQSIN

Important features:**Signal peptide:**

amino acids 1-35

Transmembrane domain:

amino acids 365-386

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern:

amino acids 371-393

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FIGURE 259

CAGGCGGGCCCCCGCGGGCAGGGCCCTGGACCCGCGGGCTCCCGGGGATGGTGAGCAAGGCCTGCTGCCCT
CGTGTCTGCCGTCACCGCAGGAGGATGAAGCTGCTGGCATGCCCTGCTGGCCTACGTCCTCTGTTG
GGCAACTCGTTAATATGAGGTCTATCCAGGAAATGGTGAECTAAAATTGAAAGCAAGATTGAAGAGATGGT
TGAACCACTAACAGAGAGAAAATCAGAGATTTAGAAAAAAAGCTTACCCAGAAATACCCACCAAGTAAAGTTTATC
AGAAAAGGATCGAAAAGAATTTGATAACAGGAGGCGCAGGGTCTGGCCTCCATCTAACTGACAAACTCAT
GATGGACGGCCACGAGGTGACCGTGGTACAATTCTCACGGCAGGAAGAGAAACGTTGGAGCACTGGATCG
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCTCTACATGAGGTTGACCAGATATACCAC
GGCATCTCCAGCCTCCCTCCAAACTACATGTATAATCCTATCAAGACATTAAGACCAATACGATTGGACATT
AAACATGTTGGGCTGGCAAACGAGTCGGTCCCCGCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC
TGAAGTCCACCCCTCAAAGTGAGGATTACTGGGCCACGTGAATCCAATAGGACCTCGGCCTGCTACGATGAAGG
CAAACGTGTTGCAGAGACCATGTGCTATGCCATCATGAAGCAGGAAGGCCGTTGAAGTGCAGTGCCAGAATCTT
CAACACCTTGGCCACGCATGCACATGAACGATGGCGAGTAGTCAGCAACTCATCTGCAGCGCTCCAGGG
GGAGCCACTCACGGTATACGGATCCGGTCTCAGACAAGGGCCTCCAGTACGTCAAGCGATCTAGTGAATGCC
CGTGGCTCTCATGAACAGCAACGTCAAGCAGCCCCTCAACCTGGGAACCCAGAAGAACACACAATCCTAGAATT
TGCTCAGTTAATTAAAAACCTTGGTAGCGGAAGTGAATTCAAGTTCTCCGAAGGCCAGGATGACCCACA
AAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGAGGCCGTGGTCCCGTGGAGGAAGGTT
AAACAAAGCAATTCACTACTTCCGAAAGAACTCGAGTACCAAGGAAATAATCAGTACATCCCCAAACCAAGCC
TGCCAGAATAAGAAAGGACGGACTGCCACAGCTGAACCTCTCACTTTAGGACACAAGACTACCATTGTACAC
TTGATGGATGTATTTGGCTTTTTGTTGTCGTTAAAGAAAGACTTTAACAGGTGTATGAAGAACAAAC
TGGAAATTCTGAAGCTGCTTAATGAAATGGATGTGCTAAAGCTCCCTCAAAACTGCAGATTG
CCTTGCACTTTGAACTCTCTTTTATGTAAGGCGTAAAGACTGATGCTCTGCGTATTTCAAGTTTTAT
CTTGCTGTGAGAGCATATGTTGACTGTCGTTGACAGTTTATTTACTGGTTCTTGTGAAGCTGAAAAGGAA
CATTAAGCGGGACAAAAATGCCGATTTATTAAAAAGTGGGTACTTAATAATGAGTCGTATACTATGCAT
AAAGAAAAATCTAGCAGTATTGTCAGGTGGTGGCGCCGGCATTGATTAGGGCAGATAAAAGAATTCTGTG
TGAGAGCTTATGTTCTTTAATTCAAGAGTTTCCAAGGTACTTTGAGTTGCAAAACTGACTTTGAAA
TATTCTGTTGGTCATGATCAAGGATATTGAAATCACTACTGTTGCTGCGTATCTGGGGCGGGGCAGGT
TGGGGGGCACAAAGTTAACATATTCTGGTTAACCATGGTTAAATATGCTATTAAATAAAATATTGAAACTCA

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FIGURE 260

MVSKALLRLVSANRRRMKLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFGSHLTDKLMMGDHEVTVDNFFTGRK
RNVEHWIGHENFELINHDVVEPLYIEVDQIYHLASPASPPNYMYNPIKTLKTNTIGTLNMLGL
AKRVGARLLLSTSEVYGDPEVHPQSEDYWGHNPIGPRACYDEGKRAETMCYAYMKQEGVE
VRVARIFNTFGPRMHMNDGRVVSNFILQALQGEPLTVYGSGSQTRAFQYVSDLVNGLVALMNS
NVSSPVNLGNPEEHTILEFAQLIKNLVGGSEIQFLSEAQDDPQKRKPDIKKAKLMLGWEPVV
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41, 101-107, 383-389

Amidation sites:

amino acids 123-127, 233-237

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FIGURE 261

GC GTGGTGC GGCGT GGGAAAT CGGTTGCCAGCCGTTACTGGTCCGCAGTCAGGG
CAT CCTCCGCAT CCTCACAT CTTCC **ATG**GCTCTGAAGAATAAATTCAAGTTATGGATC
TTGGGTCTGTGTTGGTAGCCACTACATCTTCAAATCCCATCCACTGACCCACACTT
ATAGACA ACTGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCCTCCGGCGAC
ATGAAAATACATGATTTGGATAAAGGTTAGCAAAGATGGCTAAAGCATGGCAAACCAGTGC
AAATTTGAACATAATGACTGTTGGATAAATCATATAATGCTATGCAGCTTGAAATATGTT
GGAGAAAATATCTGGTTAGGTGGATAAAGTCATTACACCAAGACATGCCATTACGGCTTGG
TATAATGAAACCCAATTATGATTTGATAGTCTATCATGCTCCAGAGTCTGTGGCATTAT
ACACAGTTAGTTGGCCAATTCTTATGTCGGTTGTGCAGTTGCAATGTGTCTAACCTT
GGGGGAGCTCAACTGCAATATTGTATGCAACTACGGACCTGCAAGGAAATTGCAAATATG
CCTCCTTACGCAAGAGGAGAATCTTGCTCTGCTCAAAGAAGAGAAATGTGTAAAGAAC
CTCTGCAGGACTCCACAACCTATTACCTAACCAAAATCCATTCTGAAGCCAACGGGAGA
GCACCTCAGCAGACAGCCTTAATCCATTCAAGCTTAGGTTCTCTGAGAATCTT**TAA**
TGTCATTTATACAAAAGAAATTCTCAAATGTTAAAATAAGGAATAGTTATTGCTTAATA

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FIGURE 262

MALKNKFSCLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNP
PAADMKYMIWDKG
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFLGFLRLIF

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site:

amino acids 119-123

N-myristoylation sites:

amino acids 103-109, 150-156, 160-166, 161-167, 175-181

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:

amino acids 136-156

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:

amino acids 166-178

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FIGURE 263

CGCCCTCCGACCCGCCCGCGCGCATTGTGGGATCTGTCGGCTTGTCAAGGTGGTGGAGGAAA
AGGCCTCCGTC**ATG**GGGATCCAGACGAGCCCCGT CCTGCTGGCTCCCTGGGGTGGGCTG
GTCACTCTGCTCGGCCTGGCTGTGGCTCCTACTTGGTCGGAGGTCCGCCGGCTCAGGTC
ACTCTCCTGGACCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCAC
AACACCAAGAGGTTCCGCTTGCCCTGCCACCGCCCACCACACTCTGGGCTGCCTGTGGC
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACTCCTGTC
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCAAGGTCTACCTGAAGGGTGTGCAC
CCCAAATTCCTGAGGGAGGGAAAGATGTCAGTACCTGGATAGCCTGAAGGTGGGATGTG
GTGGAGTTCGGGGCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTAACATTCA
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAAACTGGGAATGATTGCCGGCGG
ACAGGAATCACCCCAATGCTACAGCTGATCCGGCCATCCTGAAAGTCCCTGAAGATCCAACC
CAGTGCTTCTGCTTTGCCAACCAGACAGAAAAGGATATCATCTTGCAGGAGGACTTAGAG
GAAC TGCAAGGCCGCTATCCAATCGTTAACGCTCTGGTCACTCTGGATCATCCCCAAAA
GATTGGGCCTACAGCAAGGGCTTGTGACTGCCACATGATCCGGAACACCTGCCGCTCCA
GGGATGATGTGCTGGTACTGCTTGTGGGCCACCCCAATGGTGCAGCTGGCTGCCATCCC
AACTGGACAAACTGGCTACTCACAAAGATGCGATTCACCTACT**TGA**CATCCTCCAGCTTC
CCTGGTGTGTCGCTGCAGTTGTTCCATCAGTACTCAAGCACTATAAGCCTAGATTCT
TTCTCAGAGTTTCAGGTTTTCAAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG
AACAAATATTCCGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTGGATGCCCTCTAAA
TCTCCCGTGGCAACAGGTCCAGGAGAGGCCATGGAGCAGTCTCTCCATGGAGTAAGAAGG
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCTTGATAGCATCTTACTCACCTT
CTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGTTTACTTAAACTCACTGTTCAA
CCTATGAGCAAATCTGTATGTGAGTATAAGTTGAGCATAGCATACTCCAGAGGTGGTNTT
ATGGAGATGGCAAGAAAGGAGGAAATGATTCTTCAGATNTCAAAGGAGTCTGAAATATCATA
TTCTGTGTGTCTCTCAGCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA
AACTGCTTTGTGGCANGAACCCCTGGCTGTGCAAATAATGGGCTGAGGCCCTGTGTGA
TATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 264

MGIQTSPVLLASLGVLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKR
FRFALPTAHHTLGLPVGKHIYLSTRID GSLVIRPYTPVTSDEDQGYVDLVIKVYLGKVHPKFP
EGGKMSQYLDSDLKVGDVVEFRGPSGLLTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGIT
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPPKDWAY
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

Important features:

Signal peptide:

amino acids 1-26

N-glycosylation site:

amino acids 214-218

N-myristoylation sites:

amino acids 22-28, 76-82, 128-134, 180-186

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FIGURE 265

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAAGGCCACTGGCTTCGTTAGA
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTAGGTGACACTATAG
AATAACATCCACTTGCCTTCTCTCCACAGGTGTCCACTCCAGGTCCAATGCACCTCGGT
TCTATCGATAATCTCAGCACCGAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCGCTCAGG
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCAATGCC
TCCCCACTGCTCGGCTCCAGCTGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC
AGCTACCACCTGCAGATCCACAAGAACATGGCATGTGGATGGCGCACCCATCAGACCATCTAC
AGTGCCCTGATGATCAGATCAGAGGATGCTGGTTGTGGTATTACAGGTGTGATGAGCAGA
AGATAACCTCTGCATGGATTCAGAGGAAACATTTGGATCACACTATTCGACCCGGAGAAC
TGCAGGTTCCAACACCAAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC
TTCCTGGTCAGTCTGGGCCGGCGAAGAGAGGCCTCCTGCCAGGCATGAACCCACCCCCGTAC
TCCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGG
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCAGGGACCCCTGAACGTGCTGAAGCCCCGG
GCCCGGATGACCCCGGCCCCCTGTTCACAGGAGCTCCGAGCGCCGAGGACAACAGC
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTGAGTGAACACGCACGCTGGGGGA
ACGGGCCCGGAAGGCTGCCGCCCTCGCCAAGTTCATCTAGGGTCGCTGG

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FIGURE 266

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLHYTATARNSYHLQIHKNHGVDG
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGYDV
YHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTPIP RRHTRSAEDDSERDP
LNVLKPRARMTPAPASCQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRFAKFI

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

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FIGURE 267

GGCTGAGGGAGGCCGGAGCCTTCTGGGCCTGGGGATCCTTGCAGTGGTGGTGGAGAGAAGCGCCTGC
AGCCAACCAGGGTCAGGCTTGCTCACAGTTCTCTGGCGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC
AAATGAGGCTGCTGCGGACGGCTGAGGATGGACCCAAAGCCCTGGACCTGCCAGCGTGGCACTGAGGCAGCG
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGGACCCCTGCCAGCCCTGCCAGCCCTG
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCAGTGAGGCAAGGCTGCTTGGCAGCCACGGCCTGCAACT
CAGGAACCCCTCAGAGGCCATGGACAGGCTGCCCGCTGACGGCCAGGGTAAGCATGTGAGGAGCCGCCCG
AGCCAAGCAGGAGGGAAAGAGGCTTCATAGATTCTATTACAAAGAATAACCACCATTTGCAAGGACC**ATGAGG**
CCACTGTGCGTACATGCTGGTGGCTGGACTGCTGGCTGCCATGGAGCTGTTGCAGGCCAGGAGCAGGTTTT
GAGGGCACTGAGGAGGGCTGCCAAGAGAGTTCACTAACAGGTACAAGCGGGCGAGTCCCAGGAC
AAGTGCACCTACACCTTCATTGTGCCCGAGCAGCGGTACGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG
GTGCTCTGGAGAACCGAGTCATAAGCAGGAGCTAGAGCTGCTCAACATGAGCTGCTCAAGCAGAACGCG
ATCGAGACGCTGAGCAGCTGGTGGAGGTGGACGGCGATTGTGAGCGAGGTGAAGCTGCTGCCAAGGAGAGC
CGCAACATGAACCTCGCGGGTACGCAGCTCTACATGCAGCTCTGCACGAGATCATCGCAAGCGGGACAACGCG
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAAGACAGCCGACATGCTGCAGCTGCCAGCAAGTACAAG
GACCTGGAGCACAAGTACCAAGCACCTGCCACACTGGCCACAAACCAATCAGAGATCATCGCGAGCTTGAGGAG
CACTGCCAGAGGTGCCCTCGGCCAGGCCGTCCCCAGCCACCCCGCTGCCCGCCGGTCTACCAACCA
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGAACAGAACCTGAAGGTGCTGCCA
CCCCCTCTGCCCACTATGCCACTCTCACCGCCTCCATCTCCACCGACAAGCGTCGGGCCATGGAGAGAC
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTC
ATGCAGGTGTGGTGCAGACAGACACGACCCGGGGCTGGACCGTACCCAGAGACGCCCTGGATGGCTCTGTT
AACTTCTCAGGAACCTGGAGACGTACAAGCAAGGTTGGAACATTGACGGCAAAACTGGCTGGCCTGGAG
AACATTACTGGCTGACGAACCAAGGCAACTACAAACTCCTGGTACCCAGAGTGGACTGGTCCGGCGAAAGTC
TTTGCAGAACACGCCAGTTCCGCTGGAACCTGAGAGCGAGTATTATAAGCTGCCCTGGCGCTACCATGGC
AATGCCGGTGAACCTTACATGGCACAAACGGCAAGCAGTTCACCCCTGGACAGAGATCATGATGTCTACACA
GGAAACTGTGCCACTACCAGAAGGGAGGCTGGTGTATAACGCCGTGCCACTCAAACCTCAACGGGTCTGG
TACCGGGGGGCCATTACCGAGCCGCTACCGAGCGAGTCACTGGCTGAGTCCGAGGAGGCTCTACTCA
CTCAAGAAAAGTGGTATGATGATCCGACCGAACCCAAACACCTCCACT**TAA**GCCAGCTCCCTCCTGACCTCTC
GTGCCATTGCCAGGAGCCACCCCTGGTACGCTGCCACAGCACAAAGAACAAACTCCTCACCAGTTCATCCTGA
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTCCGAAGTCAGCAGGGATGATGGAACATGAATCGATAACGGT
GTTTCTGTCCTCCTACTTCCTCACACCAGACAGCCCTCATGTCAGGACAGGACTACAGACAA
CTCTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAAA

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FIGURE 268

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ
RVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKYQHLATL
AHNQSEIIAQLEEHQRVPSSARPVPQPPPAPPVYQPPTYNRIINQISTNEIQSDQNLKVLP
PPLPTMPTLTSLPSSTDKGWPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG
WTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVF
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYN
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRPNPNTFH

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites:

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 124-128**Tyrosine kinase phosphorylation sites:**

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites:amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,
473-479**Amidation site:**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature:
amino acids 438-451**Fibrinogen beta and gamma chains C-terminal domain proteins:**
amino acids 305-343, 365-402, 411-424, 428-458**Trehalase proteins:**

amino acids 275-292

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FIGURE 269

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTCCAGCGGCTTCTGCAACCAA
GCGGGTCTTACCCCCGGTCCTCCCGTCTCCAGTCCTCGCACCTGGAACCCAACGTCCCCGA
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGC
AGCCCTGATGCTCTGCGCCACCAGCGTCTGACTGAGCGCTCAGGGCGAACCGTGCAGTC
CAAGTCGCCGCGCTTGCGTCTGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCT
CGGCCAGGGCTGCGCAACACGGAGCGCACCCGAGTCAGCTGAGCGCTGGAGCGCG
CCTGAGCGCGTGCAGGGTCCCGCTGTCAAGGAACCGAGGGTCCACCGACCTCCGTTAGCCCC
TGAGAGCCGGTGGACCCCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAACGAGCACCT
GCGAATTAGCATCTGCAAAGCCAGTTGGCCTCCTGGACCAACGACACCTAGACCATGAGGT
GGCCAAGCCTGCCGAAGAAAGAGGCTGCCAGGATGGCCAGGAGCTGTTCCAGGTGGGAGAGGCA
TGTCAAGCCGCTGCACCGGCTGCCAGGGATTGCCAGGAGCTGTTCCAGGTGGGAGAGGCA
GAGTGGACTATTGAAATCCAGCCTCAGGGTCTCCGCCATTGGTGAAGTGCAGATGAC
CTCAGATGGAGGCTGGACAGTAATTCAAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC
CTGGGAAGCCTACAAGGGGGTTGGGGATCCCCACGGCGAGTTCTGGCTGGGCTGGAGAA
GGTGCATAGCATCACGGGGACCGCAACAGCCGCTGGCGTGCAGCTGCGGACTGGGATGG
CAACGCCAGTTGCTGCAGTTCTCCGTGCACCTGGTGGCGAGGACACGGCCTATAGCCTGCA
GCTCACTGCACCCGTGCCAGCTGGCGCCACCGTCCCACCCAGCGGCCTCTCCGT
ACCCCTCTCCACTTGGGACCAAGGATCACGACCTCCGCAAGGACAAGAACTGCGCCAAGAGCCT
CTCTGGAGGCTGGTGGTTGGCACCTGCAGCCATTCAACCTCAACGGCAGTACTTCCGCTC
CATCCCACAGCAGCGGAGAAGCTTAAGAAGGGAAATCTTCTGGAAGACACTGGCGGGCCGCTA
CTACCCGCTGCAGGCCACCAACATGTTGATCCAGCCATGGCAGCAGAGGCAGCCTCCTAGCG
TCCTGGCTGGCCTGGTCCCAGGCCACGAAAGACGGTGAECTTGGCTCTGCCAGGGATGT
GCCGTTCCCTGCCTGGCAGGGCTCCAAGGAGGGCCATCTGAAACTTGTGGACAGAGAA
GAAGACCACGACTGGAGAAGCCCCTTCTGAGTGCAGGGGGCTGCATGCGTTCCTCTGA
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGCGTGGACCAAGGGCATGGAGCTTCACT
CCTTGCTGCCAGGGAGTTGGGACTCAGAGGGACCACTTGGGCCAGCCAGACTGGCTCAA
TGGCGGACTCAGTCACATTGACTGACGGGACCAAGGGCTTGTGTGGGTCAGAGCGCCCTCAT
GGTGCAGGGCTGTGTTGTGTAGGTCCCCGGGACACAAGCAGGCGCCAATGGTATCTGGC
GGAGCTCACAGAGTTGGAAATAAAGCAACCTCAGAACAC

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FIGURE 270

MTVIRFFPAASATKRVLPVLRVSSPRTWNPNVPESPRI PAPRLPKRMMSGAPTAGAALMLCAA
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA
CQGTEGSTDLPLAPESRVDPEVLHSIQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFIEIQ
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGD
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQ
DHDLRRDKNCAKSLSGGWWFGTC SHSNLNGQYFRSIPQQRQKLKGIFWKWRGRYYPLQATT
MLIQPMAAEAS

Important features:

Signal peptide:

Amino acids 1-13

Transmembrane domain:

Amino acids 53-70

N-glycosylation site:

Amino acids 224-228

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 46-50;118-122

N-myristoylation sites:

Amino acids 50-56;129-135;341-347;357-363

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 396-409

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FIGURE 271

CGGACGCGTGGGGAAACCCCTCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG
AACAAAGATGGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGCTCCGCCGCTG
CTGCTGCTGACCATGGCCTGGCCGGAGGTCGGGACCGCTCGGCTGAAGCATTGACTCG
GTCTGGGTGATA CGCGTCTGCCACCGGCCTGTCAGTTGACCTACCCCTGCACACCTAC
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTCAATTGTCAGTT
GTGGATGATGGAATTGACTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCAATCTGATGAGCAATATGCTGCCATCTGGTTGCCAGAACATCAGCTGCCATTGCT
GAAC TGAGACAAGAACAACTTATGTCCTGATGCCAAAAATGCACCTACTCTTCCTCTAACT
CTGGTGAGGT CATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTCATGG
ACTTTTATCTCAAGCCGATGACGGAAAATAGTTATATTCCAGTCTAACGCCAGAAATCCAG
TACGCACCACATTGGAGCAGGAGCCTACAAATTGAGAGAACATCTCTAACGAAATGTCC
TATCTGCAAATGAGAAATTACAAGCGCACAGGAATTTCTGAAGATGGAGAAAGTGTGGC
TTTTAAGATGCCTCTCTTAACCTCTGGGTGGATTAACTACAACCTCTGTCCCTCTCGGTG
ATGGTATTGCTTGGATTGTTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT
GAGAAGCTGAGTATCTATGGTACCTGGAGTTATGAATGAACAAAAGCTAACAGATATCCA
GCTTCTCTCTGTGGTTTAGATCTAAACTGAAGATCATGAAGAACAGCAGGGCCTCACCT
ACAAAAGTGAATCTGCTCATTCTGAAATTTAAGCATTTCTTTAAAAGACAAGTGTAAATA
GACATCTAAAATTCCACTCCTCATAGAGCTTTAAAATGGTTCATGGATATAGGCCTTAAG
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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FIGURE 272

MAAPKGSLWVRTQLGLPPLLLTMALAGGSGTASAEAFDSVLGDTASCHRACQLTYPLHTYPK
EEELYACQRGCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL
RQEQLMSLMPKMHLLFPPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEIQYA
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTLVLSVMV
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK
VNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site:

amino acids 90-94

N-myristoylation sites:

amino acids 28-34, 29-35, 31-37, 86-92

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FIGURE 273

CCACCGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGTG
CTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACCGA
CCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT
GCAGGGTCAACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGCTCAT
AGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT
CTGTATGAACAAGAGGGCAAGCTCATCGGGAAAGCCCAGCAGGAAAGAGCAAAGACTGCGTGT
CACGGAGATCGTGTGGAGAACAACTATAACGGCCTTCCAGAACGCCGGCACGAGGGCTGGTT
CATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAACCGCGA
GGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGCCAGAAC
GAAGCAGTTCGAGTTGTGGCTCCGCCACCCGCCAGGCTTCCGCAGCCGCCAGAAC
GCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCCCACCCCTTCC
CTTCTTAATCCAAGGACTGGCTGGGTGGCAGGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC
TGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTGCCTCCCCAGGGCGGC
TGGCACAGTGCCCTTCCGGACGGGTGGCAGGCCCTGGAGAGGAAGTGTACCCCTGA
TCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCCGCTGAAAGGTAGC
GAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCTAAAATCTGCTTCTGGATCT
CCCTCAGTCTGCCCTCAGCCCCAAACTCCCTGGCTAGACTGTAGGAAGGGACTTTGTT
GTTTGTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAGAGGGTTGTCCACTCCTCA
CATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCCCGGAATAAAACCATTTCC
TGC

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FIGURE 274

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIKPGSKSKDCVFTEIVLENN
YTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGS
APTRRTKRTRRPQPLT

Important features:

Signal peptide:

Amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 275

TATTACCATATCAGATTACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTCACTCTGT
TTTATTCTCTGCCTATTGCCATCTCAGAAGTGCAGGAGCAAGGAGTCTGTGAGACTCTGTG
GGCTAGAACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAACGGCATCTGG
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAAACTCCTCCAGCTCCCACATAAACGTG
AGTTTCTGAGGAAAATCCAGCGAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC
TTGGGGTGGACAGATGCCACTGAAGAGCTTGAAAGTCAAAGAACGATTCACTGATGTCAA
GACAAGATTACAAACTTGTGTTGCACTGATGGCTGTTCCATGACTGATTGAGTGCTCTT
GCTAAGACAAGAGCAAACCCAATGGGTGGCAGAGCTTATCACATGTTAATTACAGTGTT
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGGCTTTGGTAGGCAAACACT
TCTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTCTCCCTTGCC
AAGGTTAATGAACTGTTCTTCAAATTCTACTAATGCTTGAAATTCAAATGCTGCGCAA
ATTGCAATAAAATGCTATAAA

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FIGURE 276

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRHLEGIPQAQQAETGN
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSKKHSVMSRQDLQTLCCTDGC
SMTDLSALC

Important features:

Signal sequence:

amino acids 1-18

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 107-111

N-myristoylation sites:

amino acids 3-9, 52-58, 96-102, 125-131

Insulin family signature:

amino acids 121-136

Insulin family proteins:

amino acids 28-46

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FIGURE 277

GCAGCTGGTTACTGCATTCCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTCTGCTGGATTAAAGACGG
CCCACAGACCAGAACCTCCACTATACTACTTAAAATTACATAGGTGGCTGTCAAATTCAATTGATTAGTATTGT
AAAAGGAAAAAGAAGTCTCTTACAGCTTGATCAACGGCCAAAACAAAATGCAGCTGCCATTAAAGCT
CAGATGAACAAAACTTCTACACTGATTAAAATCAAGAATAAGGGCAGCAAGTTCTGGATTCACTGAATCAAC
AGACACACAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAAATTAAACCAACGCATAGAAC
TTTTTTCTCTCTAAAACACTAAGTAAGACTTAAATTAAACACATCAACACCTCATTTACAACTCATTCAAAT
GAAGACTTTACCTGGACCCTAGGTGTCTATTCTCTACTAGTGGACACTGGACATTGCAGAGGTGGACATT
CAAAATTAAAAAAATAACCCAGAGAAGATAACCCCTCGGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA
CACATTCTGGTACCTGAACAAAGAATAACAGGGCAATCTGTGTCACACCCAAGGGCAAGATGCAAGTACCAT
TAAAGACATGATCACCAAGGATGGACCTGAAAACCTGAAGGGATGTGCTCTCAGGCAGAAGCGGGAGATAGATGT
TCTGCAACTGGTGGTGGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAGCCGTAAACAT
GAACCTCGTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACTTGAAC
TTCCCAACTGGAAAACAAATCCTCAATGTCACCACAGAAATGTTGAAGATGGCAACAAGATAACAGGAACCTAGA
GGTGAATAACGCTCCTGACTGATCTGTCAATAACCAATCTGTGATGTCACTTGTTGGAAGAACAGTGCCT
GAGGATATTTCCCACAAGACACCCATGTGTCTCCCCACTGTCCAGGTGGTGCACACATATTCTAACAG
CCAACAGTATACTCCTGGTCTGCTGGGAGGTACAGAGATTCAAGAGGGATCCAGGTTATCCCAGAGATTAAATGCC
ACCACCTGATCTGGCAACTTCTCCACAAAAGCCCTTCAAGATAACCACCGTAACCTCATCAATGAAGGACC
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGCATTGGTCAGTGGGATTATGATTAAACCTGAAAACAG
CAATGGACCAATGCACTTATGGTGTGAAAACAGTTGGACCCCTGGGGTTGGACTGTTATTCAAGAAAAGAACAGA
CGGCTCTGTCACCTCTCAGAAATTGGGAAATTATAAGAAAGGGTTGGAAACATTGACGGAGAAACTTGGCT
TGGACTGGAAAATATCTATGCTTAGCAATCAAGATAATTACAAGTTATGATTGAATTAGAAGACTGGAGTGA
TAAAAAAAGTCTATGCAAAATACAGCAGCTTCGTCAGGAAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC
TTACCAAGGGAAATGCAAGGGATTCTATGATGTGGCATATGGTAAACAAATTCCACACACTGGACAGAGATAAAGA
TATGTATGCAAGGAAACTGCGCCACTTCTATGGTAAACAGGAGGCTGGTGTACAATGCCTGTGCACATTCTAACCTAAA
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAACCAAGATGGAATTTCCTGGGCCAATACAGAGCGG
GTCATACTCCTTAAGAGCAGTTCAAGATGATGTCAGGCTATTGACTTGAAGAGAGACACTCGCCAATTAAATGA
CACAGAACTTGTACTTTCACTCTTAAATGTAATGTTACATGTTATATTACTTGGCACAATTATTTCTAC
ACAGAAAGTTTAAATGAATTTCACCGTAACTATAAAAGGGAAACCTATAATGTTAGTTCATCTGTCGTCAAT
TACTGCAGAAAATTATGTGTATCCACACCTAGTTATTAAAATTATGTTGACTAAATACAAAGTTGTTTC
TAAAATGTAATATTGCCACAATGTAAGCAAATTAGCTATATTAAATCATAAAACATGTTCAAGATA
CTTAACAATTATTTAAATCTAAGATTGCTAACGTCTAGTGAAAGGGAAACTCTAGTTTGCACATAGAAAATGTTCTT
ATGCATTATTTATAAAACAGACAGAAAATTAGGGAGAAACTCTAGTTTGCACATAGAAAATGTTCTT
CCATTGAATAAAAGTTATTCAAAATTGAATTGTCCTTACACGTAATGATTAAATCTGAATTCTTAATAATA
TATCCTATGCTGATTTCACACATGACCCATAGTATTAAATACATATCATTTAAAATAAAACCC
AAAAATAATGCATGCATAATTAAATGGTCAATTATAAAGACAAATCTATGAATGAAATTTCAGTGTATCTT
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCAATTATGTTAGTGACTGTTCTAAATCAGCAAATATTGGTATT
ACAAAAATGCAAGATAATTAGTGCTACAGATCTGAATTATGTTCTAAATTATTACTTTCTAAATT
ACTGATCTTACTACTACAAAGAAAAACCCACCCATCTGCAATTCAACATGAGAAAGTTGGACAGCTTAC
AAGTATTAGTGCTCAGAACAGGTGGACTAAAACAAACTCAAGGAACCTGTTGGCTGTTTCCGATACTGA
GAATTCAACAGCTCCAGAGCAGAACGGCACAGGGCATAGCTTACAGCTAAACTGCTAATTTCATTTACAGTGTAT
GTAACGCTTAGTCTCACAGTGTCTTAAACTCATCTTGCACATCAACAACTTACTAGTGACTTTCTGGAACAAATT
TCCTTCAAGGAATACATATTCACTGCTTAGAGGTGACCTTGCTTAATATTGTGAAGTTAAAATTAAAGA
TAGCTCATGAAACTTTGCTTAAGCAAAAGAAAACCTCGAATTGAAATGTTGAGGCAAACATATGCATGGGAAT
AGCTTAATGTGAAGATAATCATTTGACAACCTCAAAATCCATCAACATGACCAATGTTTCATCTGCCACATCTC
AAAATAAAACTCTGGTAAACAAATTAAACAAATATCCAAACCTCAAAAAAA

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FIGURE 278

MKTFTWTLGVLFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP
ICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVVDGNIVNEVKLLRKESRNM
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTEMLKMATRYRELEVKYASLTDLVNNQ
SVMITLLEEQCLRIFSRQDTHVSPPVQVVPQHIPNSQQYTPLLGGNEIQRDPGYPRDLMPP
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSQDNYKLLIELEDWSDKK
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWW
YNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation sites:

Amino acids 160-164; 188-192

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 120-124

Tyrosine kinase phosphorylation sites:

Amino acids 173-180; 387-396

N-myristoylation sites:Amino acids 70-76; 110-116; 232-238, 343-349; 400-406; 467-473;
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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FIGURE 279

CCACCGCGTCCGCGAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTGCCCGCGATCCGGC
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGGCCAGCAGCCCAGCGCGGGAGCCGGACCGCCG
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTGCTGAAGCCGAGTGCAGGAGAACGCC
CGGGCAAACGCAGGCTAAGGAGACAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGAGCAAAAGAAGCGGTGGTGGTGGCGTCG
TGGCCATGGCGCGGCTATGCCAGCTCGCTATCCGTCAGAAGAGGCAAGCCCGAGCGCG
AGAAATCCAACGCCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA
ACAAGTTAAATGTCTTCCGGTCAAACCTCTCGGCTCCAAGAAGAGGCGCAGAAGAAC
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATAAGCCGACAAGGCTACCACTTGCGAC
TGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTAAC
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTGGCAA
TGAACAGTGAGGGATACTTGTACACCTCGAACCTTCACACCTGAGTGCAAATTCAAAGAAT
CAGTGGTGGTATCTGGGTCTGAACAAAGAAGGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA
ACAAGCCTGCAGCTCATTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC
TGCACGATCTCACGGAGTTCTCCGATCTGGAGCGGGACCCAAACAGAGCAGAAGTGTCT
CTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTAGCAGTCCTTCA
CCCAAAAGTCAAATTGTCAGTGACATTACAAACAAACAGGCAGAGTTCACTATTCTATC
TGCCATTAGACCTTCTTATCCATACTAAAGC

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FIGURE 280

MAAAIASSLIRQKRQAREREKSACKVSSPSKGKTSCDKNKNLNVFSRVKLFGSKKRRRRPE
PQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLAMN
SEGYLYTSELFPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRVSGVLNGGKMSHNEST

Important Features:**N-glycosylation site:**

Amino acids 242-246

Glycosaminoglycan attachment sites:

Amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site:

Amino acids 93-100

N-myristoylation sites:

Amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop) :

Amino acids 231-239

HBGF/FGF family proteins:

Amino acids 78-94, 102-153

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FIGURE 281

CCAGGATGGAGCTGGGCCTGTATGCCATATTATTGTTCTATGCTACTAGACATGGGGGG
CTTGGTAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGCA
ACCTGGATATTCTGAGACATATTGGGGGATTCAGTGAAAAAAAGTGGGGATCCCCTCCA
TTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTGGTCTCCTGACATTGGCAGTGCCCC
AGTAGGGGTGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG
TGGATTGGCAGGAGTGTGCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTAAACCACG
TCTTGGAAATTAGTGGGTCTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA
GGGAAAGGGACGTTCAATAGGAGGAAAACTCGAGGGTGGATCCACTGAGGAGTACATA
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGTGGTAAGTGGCTGTGGAGGGG
GGTACGTGAGGGGGGGCTGGGCTTATCCTCAGGTCTGTGGTGGGCAGCGAGTCGGGG
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGGCCAGCGCGCTCCGG
CGCCTGCCGGTTGGGGGTGTCTCCTCCCGGGCGCTATGGCGCTGGCCAGTAGCCTGAT
CCGGCAGAACGGGAGGTCCCGAGCCCGGGGAGCCGGGTGTGGCGCAGCGCGCGT
GTGCCCCCGGGCACCAAGTCCCTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG
ACTGTGCGGGGGCGGCCCGCGCGGCCGGACCGCGGCCGGAGCCTCAGCTCAAAGGCATCGT
CACCAAACGTGTTCTGCCGCCAGGGTTCTACCTCCAGGCGAATCCGACGGAAGCATCCAGGG
CACCCCAGAGGATACCAAGCTCCTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCATGAATGCTGAGGGACTGCTCTACAG
TTCGCCGATTCACAGCTGAGTGTGCTTAAGGAGTGTGTTGAGAATTACTACGTCT
GTACGCCCTGCTCTACCGCCAGCGTCTGTGGCCGGCCTGGTACCTCGGCCTGGACAA
GGAGGGCCAGGTATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCACTTCTGCC
CAAGCTCCTGGAGGTGCCATGTACCAGGAGCCTCTCCACAGTGTCCCCGAGGCCTCCCC
TTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA
GCCAGCCACCAACCTGT

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FIGURE 282

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSCLCQKQLLILLSKVRLCGGRPARPD RG
PEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK
TKAAAHFLPKLLEVAMYQEPLHSVPEASPSSPPAP

Important features:**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

N-myristoylation sites:

Amino acids 54-60; 89-95; 131-137

HBGF/FGF family signature:

Amino acids 131-155

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FIGURE 283

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCAGGGAGCAGCACTGG
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCAGGGCTCTGCAACGGC
AACCTGGTGGATATCTTCTCAAAGTGCATCTCGGCCTCAAGAACGCAGGTTGCAGGC
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATTGCAGGAAGGCTACTACTTGAA
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTAAC
CTCATACCAGTGGACTACGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTACCCCTGAATGCAAGTTAAAGAA
TCTGTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT
AGAGCCTGGTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA
ACCAAACCAGCAGCTCATTTCTACCCAAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT
TTGCATGATGTTGGGGAAACGGTCCCAGCCTGGGTGACGCCAAGTAAAAGCACAGTGC
TCTGCAATAATGAATGGAGGCAAACCAAGTCACAAAGAGTAAGACAACAT**TAG**

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FIGURE 284

MAAAIASGLIRQKRQAREQHWRPSASRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR
QDPQLKGIVTRLYCRQGYYLQMHPDGALDGTDDSTNSTLFNLIPVGLRVVAIQGVKTGLYIA
MNGEGYLYPSELFPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMMNGGKPVNKSFTT

Important features:

N-glycosylation sites:

Amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins:

Amino acids 104-155, 171-198

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FIGURE 285

CGGACCGGTGGCGGACCGTGGCGGACCGTGGCGGACCGTGGCTGGTTCAGGTCCAGGTTTGCTTGATC
TCCTTTCAAAAACGGAGACACAGAAAGAGGGCTCTAGGAAAAAGTTTGGATGGATTATGTGAAACTACCC
GCGATTCTCTGCTGCCAGAGCAGGCTCGCGCTTCCACCCAGTCAGCCTCCCTGGCGTGGTAAAGAGAC
TCGGGAGTCGCTGCTCCAAAGTGCCCCCGTGAGTGAGCTCTCACCCAGTCAGCAAATGAGCCTCTCGGGC
TTCTCTGCTGACATCTGCCCTGGCGGCCAGAGACAGGGACTCAGGGGAATCCAACCTGAGTAGTAAATTCC
AGTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCAAGGTTCTCATACTTATCCAAGAAATACGGTCTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTACGTTGATGAAAGATTGGGCTTGAAGACCCAGAAGAGATGACATATGCAAGT
ATGATTTGTAGAAGTTGAGGAACCCAGTGTGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAAG
GAAAACAGATTCTAAAGGAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTATGCCACAATTACAGAAGCTGTGAGTCCTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGAAGACCTTATTGATATCTGAACCAG
AGAGATGGCAGTGGACTTAGAAGATCTATAGGCCAACTTGGCAACTTCTGGCAAGGCTTGGTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGGAGTAAGATTACAGCTGCACACCTCGTAACCTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTCTGGCCAGGTTGTCTCCTGGTTAACGCTGTG
GTGGGAACGTGCGCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCAAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAAAGACCGGTGTCAAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGCAAGGGAGCACAGGAGGATAGCCGCATCACCACCGAGCTCTGCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTTGTTGCT
TCAAGGACCTTCATCTTCAGGATTTACAGTCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCA
ACAGCTCTTTGAGAGGAGGCCAAAGGACAGGGAGAAAAGGTCTCAATCGTGGAAAGAAAATTAAATGTTGAT
TAAATAGATCACCAGCTAGTTCAGAGTTACCATGTACGTATTCACTAGCTGGTTCTGTATTCAAGTTCTTC
GATACTGGCTTAGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGTGAGCACCTGATTCCGTTGCCCTGCTTAAC
TCTAAAGCTCCATGTCCTGGCCTAAATCGTATAAAATCTGGATTTTTTTTTGCTCATATTACAT
ATGTAAAACCAGAACATTCTATGTACTACAAACCTGGTTTTAAAAGGAACATGTGCTATGAATTAAACTGT
GTCATGCTGATAGGACAGACTGGATTTTCATATTCTTATTAAAATTCTGCCATTAGAAGAAGAGAACTACA
TTCATGGTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCTTACTTATCGATAAGTCAGTTATTG
TTTCATTGTGTACATTCTTATTCTCCTTTGACATTATAACTGTGGTTCTTAATCTGTTAAATATATCT
ATTTTACCAAAGGTATTAATATTCTTTATGACAACCTAGATCAACTATTTAGCTGGTAAATTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAATACATGTATTCA
TTCTCGTATGGTGTAGAGTTAGATTATCTGATTAAAACCTGAATTGGAAATAGAATTGGTAAGTTGCAAA
GACTTTGAAAATAATTAAATTATCATATCTCCATTCTGTTATTGGAGATGAAAATAAAAGCAACTTATGA
AAAGTAGACATTCAAGATCCAGCCATTACTAACCTATTCCCTTTGGGAAATCTGAGCCTAGCTCAGAAAACAT
AAAGCACCTGAAAAGACTTGGCAGCTCCTGATAAAGCGTGTGCTGAGTAGGAACACATCCTATT
TTGTGATGTTGGTTATTATCTTAAACTCTGTCATACACTTGATATAAAATACATGGATATTCTTATGTACA
GAAGTATGTCCTAACCAAGTTCACTTATTGTAACCTGGCAATTAAAAGAAAATCAGTAAAATATTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTACTATTGAATCAAAATGTATTGAATCATCAAATAAGA
ATGTGGCTATTGGGAGAAAATTAAAAAAAAAGGTTAGGGATAACAGGTAATGCGGCC

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FIGURE 286

MSLFGLLLTSLAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF
PHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS
GTVPGKQISKGNQIRIFVSDEYFPSEPGFCIHYNIVMPQFTTEAVSPSVLPPSALPLDLNNA
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRRVVDLNLLTEEVRLYSCTP
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQLRPKT
GVRGLHKSLTDVALEHHEECDCVCRGSTGG

Important features:

signal sequence:

Amino acids 1-14

N-glycosylation sites:

Amino acids 25-29;55-59;254-258

N-myristoylation sites:

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

Amidation site:

Amino acids 229-233

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FIGURE 287

CAGCGCTGACTGCGCCGGAGAAAGCCAGTGGAACCCAGACCCATAGGAGACCCGCGTCCC
CGCTCGGCCTGCCAGGCCCGCCT**ATGGAGTTCC**CTGGGCCCTCTGGGTCTGTGCT
GCAGTCTGCCGCTGCTGATGCCACACCGTCTCTGGAACAGTTCAAATCCAAGTTCCGGA
ATGAGGACTACACCATACTATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGAGCATGAGG
AGTACCAAGCTGTGCCAGGCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG
CCAAGCATGGCCGGAGAAGCTGTCTGAGAAGATTCCAGCGCTTCACACCTTCACCCCTGGCA
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCAAACCCATCCACCAAGCATGAAGACC
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGAAAATCACTCACAGTCCTCAGGCCATGACA
ATCCACAGGAGAAGAGACTTGAGCAGATGACCCAGAGGTGGGTTCTACATAGCATCGGTC
ACAGTGCTGCCAACGCCCTTCCACTTGCTGGACTGTGCTGCTCCTTCACTTGTGCTGC
TGCAAACCCCG**TGA**AGGTGTGCCACACCTGGCTTAAAGAGGGACAGGCTGAAGAGAGGGA
CAGGCACTCCAAACCTGCTTGGGCCACTTCAGAGCCCCAGCCCTGGAACCAACTCCAC
CACAGGCATAAGCTATCACCTAGCAGCCTAAAACGGGCAATATTAAGGTTTCAACCGGAA
GGAGGCCAACCAAGCCCCAGTGCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG
GAGACAGTCCTTCCCACCATTGCTGCCTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC
CCTTAAGGCACAGTGGAGCTGAGCTGGAGGGCCACGTGGATGGCAAAGCTTGTCAAAGA
TGCCCCCTCAGGAGAGAGCCAGGATGCCAGATGAAGTGAAGGAAAGCAAGAAACAG
TTTCTTGCTTGGAAAGCCAGGTACAGGAGAGGCAGCATGCTTGGCTGACCCAGCATCTCCAG
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTGTAGCCAGGTACTGCATTCTCTCCCAT
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGCTGTGCCAACCTGTTAGAGTG
TAGCTGTAAGGGCAGTGCCATGTGTACATTGCTAGAGTGTAGCCTAAAGGGCAGGGCCC
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTCTGCTGATTCTACAACTGGAGTTT
TTTATACAATGTTCTTGTCTAAAATAAGCAATGTGTTTTTCGG

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FIGURE 288

MEFLWAPLLGLCCSLAADRHTVFVNSSNPFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHSY
YISKPIHQHEDRCLRLKVTVSGKITIHSPOAHDNPQEKRRAADDPEVRVLHSIGHSAAPRLFPL
AWTVLLLPLLQTP

Important features:

Signal sequence:

Amino acids 1-17

N-glycosylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 118-127

N-myristoylation site:

Amino acids 10-16

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FIGURE 289

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCTTC
CTTCTCCGTGCCCTACGAGGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGGGC
CTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTAACCTCCCAGGACCTATCTGGCTC
CAGCCCTCTCACCTCCCCAGTCTCTCCCCGCCTCAGCCCCATCCGTGTACACTGCCGG
GGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAGGTGGA
AACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG
GTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG
GAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCAGTGGCTG
TGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGCCTCCCTGT
CCTGGGGAACAGAGAGGCCCTGCGTGGCTACGGCAGTGTGAAGGAGAACGGACACGAGGG
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCCAGTGTGGCCTT
GGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGGCCAGTGTGGCCTT
GCCCGATGCTCAGGACCTGAGGAATCAAACGTGGTATGCAATGCAAGAACGGCTGGCCCTGCAT
CACCTCAAGTGTGTAGACATTGATGAGTGAGCTGGCACAGAGGGAGCCAACGTGGAGCTGACCAA
TTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC
ATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGCTCCAAG
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGAACAGCAGTGTAAAAC
ACCGAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAGATGGAAGGCATCTGTGTG
AAGGAGCAGATCCCAGAGTCAGCAGGCTCTCAGAGATGACAGAACGAGTTGGTGGT
CTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGCCACGCTGGCTGCTAAGGGCGAC
TTGGTGTTCACGCCATCTCATGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTCAAG
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA
CCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCCCTCCTGCTGGACACTCAGGACAGC
TTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTGCCTACAGAGCAGCCAGGTACCC
AGGCCCGGGCAGACAAGGCCCTGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT
TCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGAATTCAAAGTTTCCCTTAATGGTG
GCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTGGCCTCACAGGGTGGGCCATCACAG
CTCCCTCTGCCAGCTGCATGCTGCCAGTCCCTGTTCTGTGTTCACACATCCCCACACCCCA
TTGCCACTTATTATTCAGGAAATAAGAAAGGTCTGGAAAGTTAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 290

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT
IRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE
APDLFQWLCSDSLKLCCPAGTFGPSCLP CGGTERPCGGYQQCEGEGRGGSGHCDCQAGYGG
EACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE CGTE
GANCGADQFCVNTEGSYECRDCAKACL GCMAGPGRCKKCSPGYQQVGSKCL DVDECETEVCP
GENKQCЕНТЕГГҮРСИАЕГҮКQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFGIIICAL
ATLAAGDЛVFTAIFIGAVAAMTGYWL SERSDRVLEGFIKGR

Important features:**Signal sequence:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83; 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 291

CAGGTCCAAC TG CAC CT CGG TT CT AT CGA TT GA AT T CCCC GG GAT CCT CT AGAGA TCC CT GAC CT GAC CC AC
GCGTCCGAACACAGGTCTTGCTGCAGAGAAGCAGTTGTTGCTGGAGGGAGTGCGCGGCTGCC
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTCCAGGCACCCCTGCTGGGCAGGGAGGGCACAGGCCTGC
ACATCGAAGGTGGGTGGGACCAGGCTGCCCTGCCAGCATCCAAGTCCTCCCTGGCGCCCGTGGCCCTG
CAGACTCTCAGGGCTAAGGTCTCTGTTGCTTTGGTCCACCTTAGAAGAGGCTCCGCTGACTAAAGAGTAGC
TTGAAGGAGGCACCATGCAGGGAGCTGCATCTGCTCTGGTGGCGCTCTCCCTGGGCCTGGCTCAGGCCTGCCCTG
AGCCCTGCGACTGTGGGAAAAGTATGGCTTCCAGATGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC
CTGGCTTCCCGCCAATGTGACTACACTGAGCCTGTCAGCCAACCGGCTGCCAGGCTGCCGGAGGGTGCCTTC
GGGAGGTGCCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCT
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTGACTTTGCCTGGAGCGACCTGCACAACC
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGCAGCCTCCGAGCCTCC
GTGCTCTGCGCTCGTGCACACTCAACCACAACCGCTTGCACACATTGGCGAGGGCACCTTCACCCGCTCACCG
CGCTGTCCCACCTGCAGATCAACGAGAACCCCTCGACTGCACCTGCCATCGTGTGGCTCAAGACATGGGCC
TGACCACGGCGTGTCCATCCCGAGCAGGACAACATGCCCTGCACCTCACCCATGTGCTCAAGGGTACACCGC
TGAGCCGCCCTGCCGCACTGCCATGCTGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGC
AGCTGCGGCCTGGTTTGCTGGCACTGCACTGTGATGTGGACGGGAGCCGGCCCTCAGCTTCACTGGCACA
TCCAGATACCCAGTGGATTGTGGAGATCACAGCCCCAACGTGGCACTGATGGCGTGCCTGCTGGCACCC
CTGTGGCCAGCTCCAGCCGCCTCCAGGCCTTGCAATGGCAGCCTGCTTATCCCCACTTGGCAAGCTGG
AGGAAGGCCACCTACAGTGCCTGGCCACCAATGAGCTGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCA
CCGCCGGTGAGGGTGGTGGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAAGGGCTGCTATA
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCACTACCTCAGCCGTGCTGGGAACC
CTGAGGCTGCAGTGCAGAAGGGTCCCTGGCAGCTGCCCTGCTGGCCAAAGCCTCTCC
TCTTCTTCTCCTCACCTCTTAGCCCCACCCAGGGCTCCCTAACCTCCCTGGCCCTACCAATGCC
TTTAAGTGCTGCAGGGTCTGGGTTGGCAACTCTGAGGCCTGCATGGGTGACTTCACATTTCCTACCTCTCC
TTCTAATCTCTCTAGAGCACCTGCTATCCCCACTTCTAGACCTGCTCAAACTAGTGA
ACTAGGATAGAATTG
ATCCCCCTAACTCACTGCTCGGGTGCTATTGCTGCTAACAGCATTGCCCTGCTCTCAGGGCAGCAG
CTAACGGGGCGACGCTCTAACCAACTGGGAGAAGCCTCAGTGGGAAATTCCAGGCAGTGTGACTGTCAAGCTG
GCAAGGGCCAGGATTGGGGAATGGAGCTGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAAATGGGAGAG
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGCCTGCTCAAGCTCCCTGCTCCTTG
CTGTTTCTGATGATTGGGGCTGGAGTCCCTTGTCTCATCTGAGACTGAAATGTGGGATCCAGGATGG
CTTCCCTCCTCTTACCCCTCCCTCAGCCTGCAACCTCTATCTGGAACCTGCTCCCTTCTCCCCAACT
ATGCATCTGTTGCTGCTCCTCTGCAAAGGCCAGCCAGCTGGGAGCAGCAGAGAAATAAACAGCATTCTGATG
CCAAAAAAAAGGGCGGCCGCACTCTAGAGTCACCT

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FIGURE 292

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTTLSLSANRLP
GLPEGAFREVPLLQLSLWAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSALQL
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPDFDCTCGIV
WLKTWALTTAVSipeQDNIACTSPHVLKGTPSRLPPLPCSAPSQVQLSYQPSQDGAELRPGFV
LALHCDVDGQPAPQLHWHIQIPSGIVEITSNVGTGRALPGTPVASSQPRFQAFANGSLIP
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFLTSF

Important features:

Signal peptide:
amino acids 1-18

Transmembrane domain:
amino acids 403-418

N-glycosylation sites:
Amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site:
amino acids 319-326

N-myristoylation sites:
amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,
350-356, 394-400

Amidation site:
amino acids 355-359

Leucine Rich Repeat:
amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain:
amino acids 180-230

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FIGURE 293

ACTTGGAGCAAGCGGCGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGCCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGGCCCTCGCGAGGCAGAGGCCACGAGGAAGACCCGGTGGCTGCGCCCTGCC
TCGCTCCCAGGCAGGGCTGCAGCCTTGCCCTTGCCTGCTGCCTGAAAATGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGCTCCTCCCTGCCAGGGCAGGGCGTACGTGGAGGTCCATCT
CTAGGGCAGACAGCTCGGACCCACCCGAGACGCCCTCTGGAGACTTCCTGTGAGAACAGCAGGAC
TGGTTTCATCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGACA
TCTTGCAATTCTGGACATTGGCTCTGATGTCAAGGAGCTTCCTGTGAGAACAGCAGGAGTTCAAGAATG
AGTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTCTGCAAGAGGATGCCAGACTGTCAAGAATG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGCAGAGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTCAATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGGAGCCCCATGAGGACCATGCTTCTGTGCCAATTCAAGGACATTGAGACGCTGACCTCGTGTCC
AGAAGAAGTTGTGACGGCCACATGTCAGCACCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAAGCTACATTCTCAACTCGGATCAGACGACTTGCAAGAACATCCAGGATCTGT
GTGCCATGGAGGACCACAAGTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGACTACTGTGCCAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCAACAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGCCAAACCTGCAGCCAGTGACCAACTGTGCAC
AGCAGGACCATGCTGTGAGCAGCTGTGTGAACACCGAGGATTCCCTCGTCTGCCAGTGCTCAGAACGGCTCC
TCATCAACGAGGACCTCAAGACCTGCCCGGTGATTACTGCCCTGCTGAGTGACCATGGTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTGCCCTGCTCAGTGCTCTGAGGGACACGTCTCCGCAGCGATGGGAAGACGTGT
CAAATGGACTCTGTGCTCTGGGGACCCAGGGTGTGAACACCTCGTGTGAAGCAGTGAAAGATTGCTGCCAGTATAG
GCCAGTGTGAAAGGTTATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAGTATAG
ACCATGGCTGTGAACACATTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAACGCTGCCAGGAAGGATGTCGCAAATCAACCCACCATGGTGTGAAACACATTGTGTT
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGAAGACGGTGAAGAAAT
GCACTGAAGGCCAATTGACCTGGCTTGTGATGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTGCG
TGAAGCAGTTGTCACTGGAAATTAGATTCTTGACAATTCCCCAACCGCCTGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCACACAGAGTTCACTCTGAGAAACTCAACTCAGCAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTCACCGACGGACGGCTCAGGATG
ACGTCTCGAGTGGCCAGTAAAGCCAAGGCCAATGGTACTATGTATGCTGTGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAAAGCATCTCTATGCCAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACGTCCAAAACGGTCCAACAGCAACAGAAATCTGAGCCAGTCACCATATAATCCAAGACCTACTTT
CCTGTTCTAATTTCAGTGCACACAGATATCTGTTGAAGAAAGACAATCTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTGCAAGGCCCTTGGAAAGAAAAACACCGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCTGAGATACAGATTGAAAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACACTAATGTTAAATTTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAAATAAGCTATGCAAGTATTGTTAATATACTGTGGACAC
AACTTGCTTCTGCCCTCATCTGCCATTGTCAGTGTCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTTAGAACACTGCCCATAGGAAATGCTGTTTTGTACTGGACTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTTACTTGGAACAAGTTGGATTTTTATACAATATTAAATCACCACCTCAG

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FIGURE 294

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFIID
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAVKR
MRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI
LIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF
CINI PGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYALAEDG
KRCVAVDVYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGCEHECVN
MEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKT
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSCVSSED
SFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRK
DVCKSTTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKKCTEGFPIDILVFVIDGSKSLGEENF
EVVKQFVTGIIDSILTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAHAMKYMKGMSMT
GLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA
IEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDGRQDSPAGELPKTVQQPT
ESEPVTTINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPSGSPEEKHDQCKCENLIM
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation site:

Amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 115-119; 606-610; 892-896

N-myristoylation sites:Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;
639-645; 690-694;
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

Aspartic acid and asparagine hydroxylation sites:Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;
458-470; 540-552; 581-593

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FIGURE 295

GGCGGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCGCAGCGCTACCCGC
CATCGCCTGCCGCCGGGCCGCTGGGCTCCTGCCGCTCTGCTGCTGCCGCCGC
GCCGGAGGCCAAGAACGCCAGGCCCTGCCACGGTGCCGGGGCTGGTGGACAAGTTAA
CCAGGGATGGTGGACACCGCAAAGAACAGACTTGGCGGGAACACGGCTGGAGGAAAA
GACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATCCTGGAGGGCTGTGCGA
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGCGCAGGAGGAGCACCTGGAGGCCTGGTG
GCTGAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTGTGAAGACACTGAAAGT
GTGCTGCTCCAGGAACCTACGGTCCCAGTGTCTGCATGCCAGGGCGATCCCAGAGGCC
CTGCAGCGGGAAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGTCTGCCGGTG
CCACATGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGCTGTGAC
CAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCTGGACGAGGGCGCTGTGGATGT
GGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGACTGACAGGGAAAGGCCAGGAAA
CTGTAAGAGTGTATCTCTGGCTACCGAGGGAGCACGGACAGTGTGAGATGTGGACGAGTG
CTCACTAGCAGAAAAAACCTGTGAGGAAAACGAAAAGTGTACAAACTCCAGGGAGCTA
CGTCTGTGTGTCCTGACGGCTCGAAGAAACGGAAGATGCGCTGTGTCGCCGCCAGAGGC
TGAAGCCACAGAAGGAGAAAGCCGACACAGCTGCCCTCCCGCGAAGACCTG**TAA**TGTGCCGG
ACTTACCCCTTAAATTATTAGAAGGATGCCCCTGGAAAATGTGCCCTGAGGATGCCGTCT
CCTGCAGTGGACAGCGCGGGAGAGGCTGCCTGCTCTAACGGTTGATTCTCATTGTCCC
TTAACAGCTGCATTCTGGTTGTTCTAACAGACTTGTATATTGATAACAGTTCTTGT
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAA

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FIGURE 296

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEK
TLSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKV
CCSPGTYGPDCLACQGGSQRPCSGNGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR
NETHSICTACDESCKTCGSLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKTCVRKNENCYNTPGSY
VCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Important features:

Signal peptide:

Amino acids 1-24

N-glycosylation sites:

Amino acids 190-194;251-255

Glycosaminoglycan attachment sites:

Amino acids 149-153;155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 303-310

N-myristoylation sites:

Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;
252-258;313-319

Aspartic acid and asparagine hydroxylation site:

Amino acids 308-320

EGF-like domain cysteine pattern signature:

Amino acids 166-178

Leucine zipper pattern:

Amino acids 94-116

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FIGURE 297

AGATCTGGGCAACATTATTAACTGCTCACAGCCGGACCTGGCATCATGCTATTCCCTGAAACTACTGA
AGAACGATGGGATTAAATATTCTAAATAAATGAATTACTCAATCTCCTATGACCCTATACATAC
CACCTCAAAAAGTACATCAATATTATCATTAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATT
TTGGACAATGCAATTGTGGCACTGGCACTTTCAGTGAAGAAAAACTTGTTGCTATGGCATTCACTCATT
GACAAATGCAAGCATTCTCCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTGTGGAATCCTTAAGGGC
CCATTACATTCTGAAGAAGAAGCTAAGATGAAGGACATGCCACTCGAATTCTATGCTACTTGGCTAGCTA
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGT
TTACACCCAGATCCATTATGGAAGCATTACAGTGGATTGTAATGATTAGGTCTTTAACTTCCCAGCCA
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAATGAAACTCCACAGACTTC
CAGTAAACCTTACTGGCTGGATTATCTCAAAACAATTATCAGTCACCAATTAAATGTAAGGAGATGC
CTCAGCTCTTCTGTGTACCTAGAGGAAACAAACTACTGAACACTGCTGAAAATGCTGTCCGAACGTGAGCA
ACTTACAAGAACTCTATATTAACTACAACCTGCTTCTACAATTTCACCTGGAGCCTTATTGGCTACATAATC
TTCTTGACTTCATCTCAATTCAAATAGATTGAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAG
AGATTCTGATGATTGGGAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTTATCAATCTCGCA
GCCTGGTTAGCTGGTATAACCTCACAGAAATACCGATAACGCCCTGGTGGACTGGAAACTTAGAAAGCA
TCTCTTTTACGATAACAGGTTATTAAAGTACCCCATGTTGCTCTTCAAAGTGTAAATCTCAAATTTTGG
ATCTAAATAAAATCCTATTAAATAGAATACGAAGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGGA
TAAATAATGCTGAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAAG
CTACTAACACCCCTAGATTGTCTTACATTCCCCATGCATTTCAGACTCCCCAAGCTGGAATCACTCATGC
TGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGAGTCTGCTGCCAACCTCAAGGAAATCAGCATA
ACAGTAACCCCATCAGGTGTGACTGTGTACCCGGATGAACATGAACAAACCAACATTGATTATGGAGC
CAGATTCACTGTTGGTGGACCCACCTGAATTCAAAGGTCAAATGTTGGCAAGTGCATTCAAGGACATGA
TGGAAATTGCTCCCTTTAGCTCTGAGAGCTTCTTCTAATCTAAATGTTAGAAGCTGGAGCTATGTT
CTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTGGTAAAAACTCTTG
CTAATACCTGACAGACAAGTCTATGTCATTCTGAGGGAACACTAGATAAAATGGCTAACTCCAAAGAAG
GGGGTTTATATACTTGTATAGCAACTAACCTAGTGGCCTGACTTGAAGTGTGTTATGATCAAAGTGGATGGAT
CTTTTCCACAAGATAACAATGGCTTTGAATTAAAGAGATATTCAAGGCCATTCAAGTTGGTGTCT
GGAAAGCAAGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGCAAGACTGAAAATTCTCATGCT
CGCAAAGTCTCGAATACCATCTGATGTCAAGGTATAATCTTACTCATCTGAATCCATCAACTGAGTATAAA
TTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAATGTGTAAATGTCACCACCAAGGTTGCACC
CTGATAAAAAGAGTATGAAAAGAATAATACCAACACTTATGCCCTGTCTGGAGGCCTCTGGGATTATTG
GTGTGATATGTCTTATCAGCTGCCTCTCCAGAAATGAACCTGTGATGGTGACACAGCTATGTGAGGAATTACT
TACAGAAACCAACCTTGCATTAGGTGAGCTTATCTCCTCTGATAAAATCTCTGGGAAGCAGGAAAGAAAAAA
GTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATGTCTTCAAAACCCACCAAGGAAACCTA
CTCCAAAAATGAAC

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FIGURE 298

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
PARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNAVGLENLESISFYDNRLIKVP
HVALQKVNLKFQDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPDLRKIE
ATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHSNPIRCDCVIRW
MNMMNKTNIRFMEPDSDLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS
FHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVKTENSHAAQ
SARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVT KGLHPDQKEYEKNNTTLM
ACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:

Signal sequence:
amino acids 1-22

Transmembrane domain:
amino acids 633-650

N-glycosylation site.
amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.
amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.
amino acids 570-579

N-myristoylation site.
amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.
amino acids 277-280

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FIGURE 299

GCTGTGGAACCTCTCACGCGACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGGACAGAGCG
CCCCGGCCGCCTGATGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGACGGCGTCGGAACCAT
ACCATGCCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTATCGTCGCGGTCTGCTGCCA
GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATTACACCAACGCTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTGTAATCAGATAAAAACATAAAAGTTCTGCACCATGACC
AGAGACACAGTGTGTCACTGTAAAGAAGGCACCTCCGGAATGAAAACCTCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTACGTCTGGATGAT
ATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGAAACCCCAGCTGCTGAAGAGACA
ATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGG
ACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCAGCTGCT
GAAGAGACAATGACCACCAGCCGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
AGCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTGTTTGAAAGACTTCACTGTGGAAGAAATTCTCTTACCTG
AAAGGTTCAAGGTAGGCCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVNCTSDDIQCVEFGANATVETPAAEETMNTSPGT PAPAAEETMNTSPGT
PAPAAEETMTTSPGT PAPAAEETMTTSPGT PAPAAEETMTTSPGT PASSHYLSCTIVGIIIVLI
VLLIVFV

Important features:

Signal peptide:

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTGAAATCCACAAAGTTCATGTAATGAAAAGAAATACATAATTTAAT
TCAACCCGAGTGTGTTCCAAGAAGATTGTATTGCTTAAATTGCTACAGTAATTCAAGAGACAGC
GCCCTGTCTGGACACAGAGTTACTGTGGATTAAAGAGACTCAGTTAAAGAATTAGGAATT
TCTGATTCAATTAAAGGATTACAAATTCAACCCCTGAAAACCTAAAGCAAATTGAACAGG
AAAAAAAAAAAAGAAG**T**GGGTTTTAAGTCAATATATGTTTTCTTTGGAGTC
AAAGTACATTGCCAATATGAAACTTATCAGTGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTCCCATTCTGTCAAAATGTAGACTACGGAGTCCCTTCATCAGTAT
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAACTAACCTTCATCATCAATGTACTGTGAT
AATCGCAAACACTCAAGACTATCCAAATATTCCGATGCACATTCAAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCAATTCAATGCAACTCATCTTAAAGAAATTAAAC
CTCAGCCACAACAAAATTAAATCTCAAAAGATTGATTATGGTGTGTTGCTAAGCTTCAAAT
CTACTACAACTTCATCTAGAGCATAATAATTAGAAGAATTCCATTCCCTTCTCAAATCT
CTGGAAAGACTCCTTCTGGTTACAATGAAATCTCAAAACTGCAGACAAATGCTATGGATGGG
CTAGTAAACTTGACCATGCTGATCTGTTATAATTATCTTCATGATTCTGCTAAAAGAC
AAAATCTTGCCAAAATGGAAAAACTAATGCAGCTAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTGCCTTCTTCACTTATGTATCTGCTTTAGAAAATAATTCAATTCTTCT
ATACCCGAAAATACTCGACAAACTCCTCAAAACTCTAACTCTAAGAATGTCACACAACAA
CTACAAGACATCCCATAATAATTCTTAAATCTTCCAACATTGTTAGAAACTCAGTGTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCAAGAAATTGGAACACCTATAACCTACAAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGTGTCCTCTATTGACCCACTACATTACCACCAT
TTAACATACATTGTTGGACAAAATAACTAAAAGAACCAATAAGCTCATACATCTTCTTC
TGCTTCCCTCATACACACTATTATTGGAACACGAAGCAACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTCAGGAGATTCCAGATGATGATGATGAAAGTGAAGATCACGAT
GATCCTGACAATGCTCATGAGAGCCAGAACAGAAGGAGCAGAAGGGCACTTGACCTTCAT
TATTATGAAAATCAAGAA**T**AGCAAGAAACTATATAGGTATACACTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTAAAGTTGTTGGTGCATCTGCATCTTCATAGGATTAG
AACTTACTCAAAATAATGTAATCTTAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAAACGTTAATGGTTCTTATGCTCTTTAAATATAGAAATATCATGTTAAAGAAAAAA
AAAAAAA

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FIGURE 302

MGFLSPIYVIFFFGVVKHCQYETYQWDEDYDQEPPDDYQTGFPFRQNVDYGVPFHQYTLCV
SECFCPTNFPSSMYCDNRKLKTIPNIPMHIQQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPFPLPKSLERLLLGYNEISKLQTNAMDGLVNLT
MLDLCYNYLHDSLLDKIFAKMEKLMQLNLCSRLESMPGLPSSLMYLSLENNSSIPEKY
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNEIEKM
NLTVMCPSIDPLHYHHLYIRVDQNLKEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRRFPDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:

N-glycosylation sites:

Amino acids 113-117; 121-125; 187-191; 242-246; 316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275; 300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168; 217-239

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FIGURE 303

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTACCA
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGCATGAATCTGGT
AGACCTGTGGTTAACCGTCCCTCTCCATGTGTCTCCTCACAAAGTTTGTCTTATGAT
ACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGGGTTT
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGGACCTCCA
TCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCATGCCTCAA
AGGAGTAGCTGAAACCTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG
TAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA
CCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCATTGGCTGGTT
CACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCGGAGACA
CCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGTATGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAAGTAGTTGCGATTGCA
GTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAAACTTGTATTCAGTT
TTTTGAATTATGCCACTGCTGAACTTAACAAACACTACAACATAAAATAATTGAGTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTAAATTAAAAGCAAATAAAAG
CTTAACCTTGAACCATGGGAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDLP
PETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLNRIQ
SVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGRPFNAA
NDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKKADEP
DDISTVV

Important features:

Signal sequence:

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51; 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43; 45-51; 110-116

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FIGURE 305

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTTCCACTTGTGAATTGTTCC
ATACTCAAATTGCACCAAGACACCTTGTCTCCAAATGCAAATGTGAATGCAATGGAATTGAAGCCTGCT
ATTGCAACATGGGATTTCAAGGAAATGGTGTACAATTGTGAAGATGATAATGAATGTGGAAATTAACTCACT
CCTGTGGCGAAAATGCTAATTGCACTAACAGAAGGAAGTTATTGTATGTGTACCTGGCTTCAGATCCA
GCAGTAACCAAGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAATGTGAATGCAAACCTGCCATTAG
ATAATGTCTGTATAGCTGCAAATATTAACTTAAACAAAAATCAGATCCATAAAAAGAACCTGTGGCTTGC
TACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGATAATTACATATTAGAAATTAGCTG
AATCATCTTCAATTACTAGGTACAAGAACACTATCTCAGGCAAGGACACCCCTTCTAACTCAACTCTTACTG
AATTGTAAAACCGTGAATAATTGTTCAAAGGGATACATTGTAGTTGGGACAAGTTATCTGTGAATCATA
GGAGAACACATCTTACAAACATGCAACTGTGAAACAAGCTACTTAAAGGATATCCCAGAGCTTCAAAGA
CCACAGAGTTGATACAAATTCAACGGATATAGCTCAAAGTTCTTGTATTGATTATATAACATGAAACATA
TTCATCTCATATGAATATGATGGAGACTACATAATTATTTCAAAGAGAAAAGCTGCATATGATTCAAATG
GCAATGTTGCAGTTGCATTTTATATTATAAGAGTATTGGTCCTTGCTTCATCATCTGACAACCTCTTATTGA
AACCTAAAATTATGATAATTCTGAAGAGGAGGAAGAGTCATATCTTCAGTAATTCTAGTCTCAATGAGCTCAA
ACCCACCCACATTATATGAACCTGAAAAAATAACATTACATAAGTCATCGAAAGGTACAGATAAGGTATAGGA
GTCTATGTGCATTGGATTACTCACCTGATACCAGAACATGGCAGCTGGCTTCAGAGGGCTGTGAGCTGACAT
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTGCAATTGATGTCCCTGGCTT
CCATTGGTATTAAAGATTATAATATTCTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTTGTCTT
CCATATGCATTTCACCTCTGGTCTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAAATTTGCT
GTAGCTATTCTGCTGAACCTGTTTCTGTGGATCAATAACAAATACTAATAAGCTCTGTGTTCAATCA
TTGCCGACTGCTACACTACTCTTTAGCTGCTTGCACTGGATGTGCATTGAAGGCATACATCTCTATCTCA
TTGTTGTGGGTGTCATCTACAACAAGGGATTTTGCAACAAGAATTTTATCTTGGCTATCTAAGCCCAGCCG
TGGTAGTTGGATTTCGGCAGCACTAGGATACAGATAATTGCGACAACAAAAGTATGTGGCTTAGCACCAGAA
ACAACATTATTGGAGTTTATAGGACCGATGCCTAATCATTCTGTTAATCTCTGGCTTTGGAGTCATCA
TATACAAAAGTTTCTGTCACACTGCAGGGTTGAAACAGAAGTTAGTTGCTTGGAGACATAAGGTCTTGTGCA
GAGGAGCCCTCGCTTCTGGCTTCAGCAGCAACTGGATCTTGGGTTCTCATGTTGCAACGCATCAG
TGGTTACGTTACCTCTCACAGTCAGCAATGCTTCCAGGGATGTTCAATTCTGTGTTTATTCTGTGTTTAT
CTAGAAAGATTCAAGAAGAATTACAGATTGTCAAAATGCCCCCTGTTGGATGTTAAGGTAAACAT
AGAGAATGGGATAATTACAACGTGACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAAATGACT
CATCAAATTATCCAATTATTAACTACTAGACAAAAGTATTTAAATCAGTTTCTGTTATGCTATAGGAAC
GTAGATAATAAGGTAATTATGTATCATATAGATATACTATGTTTCTATGTGAATAGTTCTGCTAAAATA
GTATTGCAAGATATTGGAAAGTAATTGTTCTCAGGAGTGATATCACTGCACCCAAAGGAAAGATTCTTCTA
ACACGAGAAGTATATGAATGCTGTGAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAAC
AGTCCCCCTACCAACCTCGTAATGAGCTCATTACAGAAAAGTGAACATAAGAGAAATGAAGGGCAGAATATCAA
CACTGAAAAGGGAAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGACTAGCTGAGAAATTGTTGACAT
AAAATAAGAATTGAAGAACACATTACCAATTGTGAATTGTTCTGAACTAAATGTCCACTAAAACAAC
AGACTTCTGTTGCTAAATCTGTTCTTTCTAATATTCTAAAAAAAAAAAGGTTACCTCCACAAATTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 306

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTEGSYYCMCVPGFRSSNQDRFITNDGTVCIENVNANCHLDNVCIAANINKTLKIRSIKEPVALLQEYVRNS
VTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKL
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFFDSYNMKHIHPHMNMGDYINIFPKRKAAYDSNGNVAVAFL
YYKSIGPLLSSSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFVN
SPDTMNGSWSSEGCELYTSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLGIIISLICLAICIFTW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYN
KGFLHKNFYIFGYLSPA VVVGFSAA LGY RYY GTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHT
AGLKPEVSCFENIRSCARGAL ALLFLLGTTWIFGVLVHV HASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEY
YRLFKNVPCCFGCLR

Important features:

Signal peptide:

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450; 494-515; 573-594; 619-636; 646-664

N-glycosylation sites:

Amino acids 15-19; 21-25; 64-68; 74-78; 127-131; 177-181;
188-192; 249-253; 381-385; 395-399

Glycosaminoglycan attachment site:

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44; 670-677

N-myristoylation sites:

Amino acids 38-44; 50-56; 52-58; 80-86; 382-388; 388-394;
434-440; 480-486; 521-527

Aspartic acid and asparagine hydroxylation site:

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCAGCGCCCAGCCGTCTAACGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGGCGCCAGGTTGCGTAGGTGCGCACGAGGAGTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGC
CCGGAGGAGCGCCTCCCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGTCAGCAGGGCACTGCAGGGCGA
GGCCGGGCCGCCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCATAGGATTGA
AGAAGATATCCTGATTGTTCAAGAGGGAAAATGGCACCTTTACACATGATTCAAGAAAAGCGAACAGAGAAT
GCCAGCTATTCCCTGTCAATATCCATTCCATGAATTTCACCTGCAAGCTGCAGGGCAGGCAGAAATACTTCTATGA
ATTCCCTGTCCTTGCCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGT
GCCTCACAAGGCATCAGTTGTTCAAGTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTAAACATG
TCAACAAGCTGAGTGCCAGGCAGGTGCCGAAATGGAGGCTTTGTAATGAAAGACGCATCTGCAGTGTCTGA
TGGTTCCACGGACCTCACTGTGAGAAAGCCTTGTACCCACGATGTATGAATGGTGGACTTGTGACTCC
TGGTTCTGCATCTGCCACCTGGATTCTATGGAGTGAACTGTGACAAAGCAAACGTCAACCACCTGCTTAA
TGGAGGGACCTGTTCTACCCCTGGAAAATGTTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA
ATGCCCAACCCCTGTCGAAATGGAGGTAATGCATTGGAAAAGCAAATGTAAGTGGTCCAAAGGTTACCGGG
AGACCTCTGTTCAAAGCCTGCTGCGAGCCTGGCTGTGGTCACATGGAACCTGCCATGAACCCAAACAAATGCCA
ATGTCAAGAAGGGTGGCATGGAAGACACTGCAATAAAAGGTACGAAGGCCAGCCTCATACATGCCCTGAGGCCAGC
AGGCCAGCTCAGGCAGCACACGCCCTCACTAAAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATT
CATCTGGTGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTGTGAAACCTTCACTGTGTT
GAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAAATTATTAGCTTCATTATAAATCACTGAGC
TGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAGCATGATGGTATAGATTCTGTTCACTGCT
TTGGGACAGATTTATATTATGTCAATTGATCAGGTTAAATTCAGTGTGAGTGGCAGATATTTCAAAAT
TACAATGCATTTATGGTGTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAA
GAATTGGATGGTCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAGATATTAGATGTTGTTAC
ATTTTAAAAATTGCTTTAATTTAAACTCTCAATACAATATATTGACCTTACCAATTATCCAGAGATTCA
GTATTAAAAAAAAAAAATTACACTGTGGTAGTGGCATTAAACAATATAATATTCTAAACACAATGAAATAG
GGAATATAATGTATGAACCTTTGCATTGGCTGAAGCAATATAATATTGTAACAAAACAGCTTACCT
AATAAACATTTATACTGTTGTATGTTAAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAA

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FIGURE 308

MARRSAFPAAALWLWSILLCLLRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQRMPAI PVNIHSMNFTWQAAGQAELYF EFLRSLDKGIMADPTVNPLLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGCRNG
GFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN
GGTCFYPGK CICPPGLEGEQCEIS KCPQPCRNGGK CIGKS KCKCSKG YQGDLC SKPVCEPGCG
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92; 245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190; 185-191; 189-195; 315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210; 230-242; 262-274; 294-306; 326-338

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FIGURE 309

CCACACGCGTCCGGTCTCGCTCGCGCAGCGGGGGCAGCAGAGGTGCACAGATGCC
TTAGACTGGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGACT
CTTGCAGCTGGATGCCCTCTGTGGATGAAAG**A**T**G**TATCATGGAATGAACCCGAGCAATGGAG
ATGGATTCTAGAGCAGCAGCAGCAGCACCTCAGTCCCCCAGAGACTCTTGGCG
TGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTTCGATG
ACCTCAAGTGTGTGCTGACCCGGCATTCCGAGAATGGCTCAGGACCCCAGCGGAGGGG
TTTCTTGAGGCTCTGTAGCCCATTCACTGCCAAGACGGATTCAAGCTGAAGGGCGTA
CAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGTATAATTCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTGTGATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCCTGAGACCTCTAGCCTCTTAAATGGCTATGTAACATCTCTGAGCTCCAGACCTCCT
TCCCGGTGGGACTGTGATCTCTTATCGCTGCTTCCGGATTAAACTGATGGGTCTGCC
ATCTTGAGTGCCTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTGCCTTGCTCTGGAAG
CCCAAGTGTCCACTACCTCAAATGGTGAGTCACGGAGATTGCTTGCCACCCGGCCTT
GTGAGCGCTACAACCACCGAACTGTGGTGGAGTTTACTGCGATCCTGGCTACAGCCTCACCA
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGACCACGTGGAAGATTG
CGTTCACGGCAACCAGTGTGCTGGTGTGCTCGTCATCCTGGCCAGGATGTTCCAGA
CCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCGGAGTTCCACGGAGTGA
TTGTGGTGGTAGACGGCGTGCCTCATGCTCCGTCATGACGAAGCTGTGAGTGGCGCT
TGAGTGCCTTAGGCCCCGGTACATGGCCTCTGTGGGCCAGGGCTGCCCTACCGTGGACG
ACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGACACAGGCCAGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTGTGAGCTGCTCAAAGTCTGTATTCA
AAGAGAGCACCCACCCTGCTCGGACAACCTGACATAATTGCCAGCACGGCAGAGGAGGTGG
CATCCACCAAGGCCAGGCATCCATCATGCCACTGGGTGTTCTAAGAAACT**G**ATTGATTA
AAAAATTCCCAAAGTGTCTGAAGTGTCTTCAAATACATGTTGATCTGTGGAGTTGATT
CTTCCCTCTTGTGGTTTAGACAAATGTAACAAAGCTCTGATCCTTAAATTGCTATGCTG
ATAGAGTGGTGGAGGGCTGGAAGCTTGTCAAGTCCTGTTCTTGACACAGACTGATTAAA
AATTAAAAGNAAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP
ENGFRTPSGVFFEGSVARFHQCQDGFKLKAGATKRLCLKHFNGLGWI PSDNSICVQEDCRIPO
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPICGCLRPLASSNG
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS
HGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASNDPDIIASTAEVASTSPGIHHAHWVLFLRN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG
AGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAGGCT
CGTCCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTATGCGTGCCTCACCTGGCGCT
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCAACGCCCTGGCCTCCCTGCCCTGCACCGCGTCAGTGACT
GCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCACGCCACCCAGACT
GTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAGGGGATGCCA
CAACCATGGGGCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCCACAACCATGG
GGCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTCCTGCGGAG
ACCAGTCTGGAAGGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGCTAGTCAAGCC
TGGTCACCGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCCAGGAGCGCCTCCGCCACTGG
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACGACTCGCTGCCTGAG
GACAAGCACTGCCACCAACCGTCACTCAGCCCTGGCGTAGCCGGACAGGAGGAGCAGTGA
TGC GGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTCTGCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACGTGAGGGCTGCCAGGCAGC
TCCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTGCCCGTCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT
SGLCVPLTWRCRDLDCSDGSDEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKLRN
CSRLACLAGELRCTLSDDCIPLTWRCGDGHPDCPDSSDELCGTNEILPEGDATTMGPVTLES
VTSLRNATTMGPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVATLLLLSW
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGCGTCCGGCGGTGCAGAGCCAGGAGGCGGAGGCCGGCAGCCTGGCCCCAGCCCACAC
CTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCACACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC
TTGGCTCTGGGTGCCAGCAGGGTCTGGCGCCGGGAGCTAGCACCGGTCTGCACCTGCCGGCATCCGGAC
GCCGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGTGCCGACGACTGTGCCCTGCCCTACCTG
GGCGCCATCTGTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGACTTCTGC
CTCGCGTGCCACCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTGGAAACG
TACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATAAAGC
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGGCCCTCTGGGCATGACCCTGAGGGCAT
TCGCTACCGCCTGGCACCATCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCC
AGGGGAGGTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTCTGACCAAGG
CAACTGTGCAGGGCCTGGGCCCTCTCCACAGCAGCTGTGGCATCCGATCGTCTCAATCCATTCTGGGACA
CATGACGCCCTGCTCTGTCGCCCAAGAACCTGCTGTTGTGACACCCACCAGCAGCAGGGCTGCCGGTGGCG
TCTCGATGGTGCTGGTGGTCTGCGTCGCCAGGGGTGGTGTGACCACTGCTACCCCTCTGGGCCGTGA
ACGAGACGAGGCTGGCCCTGCCCCCCCTGTATGATGACAGCCGAGCCATGGTCGGGCAAGGCCAGGGCAC
TGCCCAC TGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGCTACCGCCTGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGCTCAAGGCCCATGGAGGTGATGAGGACTTCTT
CCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGAGGCCAGAGAGATACGCCGGCATGGAC
CCACTCAGTCAAGATCACAGGATGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCC
CAACTCCTGGGGCCAGCCTGGCGAGAGGGCCACTTCCGATCGTGCAGCGTCAATGAGTGCACATCGA
GAGCTCGTGTGGCGTCTGGGCCGTGGCATGGAGGACATGGTCATCACTGAGGCTGGGGCACCAAGC
GGGGTCCGGCCTGGATCCAGGCTAAGGCCGGCGGAAGAGGCCCAATGGGCGGTGACCCAGCCTGCCGA
CAGAGCCCAGGGCGCAGGCCAGGGCGCTAATCCGGCGGGTCCGCTGACGCAAGGCCCTGG
AGCCCGGGCAGCGAGACTGGCGGAGCCCCCAGACCTCCAGTGGGACGGGCTGGCCTGGGAAGAG
CACAGCTGCAGATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGGCC
CAATACCCACCCAAATCCGTATTCTTTTTTTAGACAGGGCTTGCTCCGTTGCCAGGTTGGAG
TGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGGTCAAGTGACCCCTCCACCTCAGCCTCTCAAG
TAGCTGGACTACAGGTGACCAACCACCTGGCTAATTGTATTGTAAAGAGGGGTCTCACTGTGT
TGCCCAGGCTGGTTCGAACCTCTGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGATTGCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTAAAATAAAA
CCAAAGTATTGATAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDCA
LPYLGAICYCDLFCNRTVSDCCPDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415**N-myristoylation site.**amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448**Amidation site.**

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCTGGTGGGCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCAGGAC
CCAGGGAACTGGAAGCCAGCAAAGTTGTCCCTGCCAGTTGTCCGGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCTCAAGGCCACCTGGACCACCAGGCAAGATGGGCCCA
AGGGTGAGCCAGGCCAGAAACTGCCGGAGCTGTTGAGCCAGGGGCCACCTTGAGCGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGCCCTCCAGTCTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTCTGTGGATTCTCCGCTTGGT
CCTCCTACAGAGCAGGTTGGAACCAAGAGTCTGAATTCTGGCTGGAAATGAGAATTG
ACCAGCTTACTCTCCAGGGTAACGGAGCTGCCAGGACTGGAAAGACTTAATGGTAACC
GTACTTTCGCCACTATGCGACCTTCCGCCCTCGGTGAGGTAGACCACTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGCAGTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG
CCCACAAATATGGCATTGACTGGCCTCAGGCCGTGGTGTGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATAGGGCACTCTGGCAGCCAGTGCCTTATCTCCTGTACAGCTCCGG
ATCGTCAGCCACCTGCCCTTGCCAACCACCTTGCTGCCTGTCCACATTAAAAATAAAAT
CATTTAGCCCTTC

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKQEHPSCPGPRELEASKVVLPLSCPAGSPGEKGAPGPQG
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCPEGRALPVFCDMTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQTLQGNWELRVELEDFNGNRTFAHYATFRL
LGEVDHYQLALGKFSEGTDASLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

Important features:

Signal peptide:

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCAGGGCGGGGGTGTGCGGGGCCAACCCCCAGGG**AT**
GCTCCCCTGCCTCCTGCCTACCCGGGTCTACTGCTCTGGCGCTGCTACTGTTGCTCTT
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCCGGATGTCAACGAGTGTCTGACCATCCCTGAGGC
CTGCAAGGGGGAAATGAAGTGCATCAACCACACTACGGGGCTACTTGTGCCTGCCCGCTCCGC
TGCCGTCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC
CAACCCCTGCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCCAGGCCCTGCACGACTGTCGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCGAGTGTGTGGACATAGACGAGTGCCG
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCCTGGCTCCTCCGCTGCCAGTGCAGGCC
GGGCTTCCAGCTGGGGCTAACAAACCGCTCTGTGTTGATGTGAACGAGTGTGACATGGGGC
CCCATGCGAGCAGCGCTGCTCAACTCTATGGGACCTTCCTGTGCGCTGCCACCAGGGCTA
TGAGCTGCATGGGATGGCTTCTCCCTGCAGTGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTCTCCTGCCACTGCCACAGGGTTACCA
GCTGCTGCCAACCGCTCTGCCAACGACATTGATGAGTGTGAGTCTGGTGCACCGAGTGC
CGAGGCCAACCTGTGTCACCTCCATGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTGCCCGCCTCCAACCCCTATGTC
AGAGCAGCCTCATCCATTGTGACCCGCTACATGACCATCACCTCGGAGCGAGCGTGCCGC
TGACGTGTTCCAGATCCAGGCACCTCCGTCTACCCGGTGCCTACAATGCCCTTCAGATCCG
TGCTGGAAACTCGCAGGGGGACTTTACATTAGGCAAATCAACAAACGTCAAGCGCCATGCTGGT
CCTCGCCCGGGCGGTGACGGGCCCCCGGGAGTACGTGCTGGACCTGGAGATGGTACCATGAA
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTGTAGGGGCCTACAC
CTTC**TGA**GGAGCAGGAGGGAGCCACCCCTCCCTGCAGCTACCCAGTGTAGGGAGCCTGTTGTGA
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCCTGGTGGCTGAGGTGGCGGGTC
ACACTGCAGGAAGCCTCAGGCTGGGCAGGGTGGCACTGGGGGGCAGGCCAAGTTCACCTA
AATGGGGGTCTCTATATGTTCAGGCCAGGGCCCCCATTGACAGGAGCTGGAGCTCTGCAC
CACGAGCTTCAGTCACCCCGAGAGGGAGAGGGAGGTAAACGAGGAGGGCGGACTCCAGGCC
CCAGAGATTGGACTTGGCTGGCTTAAGAAACTCCACTCTGGACAGCGCCAG
GAGGCCCTGGGTCCATTCTAAACTCTGCCTCAAACGTACATTGGATAAGCCCTAGTAGTT
CCCTGGGCCTGTTTCTATAAAACGAGGCAACTGGAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLGSASPQDSEEPDSYTECTDGYEWPDSQHCRDVNECLTIPE
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSY
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSEAQTCVNFHGGYRCVDTNRC
VEPYIQVSENRCLCPASNPLCREQPSSIVHRYMTITSERSVPADVFQIQATSVYPGAYNAFQI
RAGNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVRLTVFGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCGACACCATGTACCTGCCCTGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGTATGTGCACGGCGGCTG
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGCAGGGCCTGGTCTGCCAGCCCCGG
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCCTTGCGAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCCTGTATCGGAAGGGGAGACCTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTCACCTGCGTGCCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGGGAC
TGCCCCCACCCCAGGAGGGTCGAGGTCTGGCAAGTGTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCTTCCAGCCAAGGACCCAGTTTCTGGCCTGTCT
TCCCTGCCCTGGTGTCCCCTGCCAGAATGGAGCACGCCCTGGGACCCGTCTGACCA
TGTGGGCTGGCATGCCACCCGGGTCTCAACCAGAACCGCTCTGCCACTGGAGACCCAG
CGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCCTCCAGGGTCGAGTCCACAAAACAGTGC
TTCTAGAGCCGGCTGGATGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGCTGATGGAAGATGGTCCGTGCCAGGCCCTGGCTGCAGGCAACACTTAGC
TTGGGTCCACCATGCAGAACCAAATTAAACACGCTGCCTGGTCTGTCTGGATCCGAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCTTCCTCTAACTCACTGCCTAGGAGGCTGCCAAGGT
GTCCAGGGCCTCTAGCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTCTCCGACTTCCCCTGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGCTGGACTGCCATTCTGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGCTGCCTTCTGGAGTTGTAAAATTGTTCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVDGCGCCRVCARRLGE
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEDG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSL
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRLCLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;
167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

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FIGURE 321

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FIGURE 322

MMGLSLASAVILLASLLSLHLGTATRGSDISKTCCFQYSHKPLPWTWVRSYEFTNSCSQRASI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine) .

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGCCGAAGGCAGCCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA
TGCCCAGCCCCCTCCTGGCTGCTGGCAGCCCACCTCTCTGCTGGTCTGGCTCAGTGCTGTCAAGGCTCGGCCA
CGGGCTGCCGCCGCCGCTGCCAGTGCCTCCGCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACGCCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACG
AGTTGCCAGCTTCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGGCCGTGGAGGCCGGCCT
TCAACAACCTCTCAACCTCCGGACGCTGGCTCCGCAGCAACCGCCTGAAGCTCATCCGCTAGGCGTCTTC
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGATGTTATCCTACTGGACTACATGTTCAAG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCCGTGCCCACCTGC
ACGGCCTCATCGTCCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGCTGTAC
GACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAACGTGCTCTACGGCCTCAACC
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCGTCCGCCACCTAGTCTATCTCC
GCTTCCCTCAACCTCTCCTACAACCCCACATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGGGGGGGGAGCTGGCGTGGTGGAGCCCTATGCTTCCCGCGGCCCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGGAGACACTCA
TCCTGGACTCCAACCCGCTGCCCTGCGACTGTCGGCTCTGTGGGTGTTCCGGCGCCGCTGGCGCTCAACTTCA
ACCGGAGCAGCCCACGTGCCACGCCAGTTGTCAGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC
TGCCCAACTACTTCACCTGCCCGCGCCGATCCGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCC
ACACGGTGCAGTTGTGTCGGGCCGATGGCGACCCGCCGCGCCATCCTCTGGCTCTCACCCGAAAGCACC
TGGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGTACGCCAGGTAC
AGGACAACGGCACGTACCTGTGCATCGCGCCAACGCCGGCGAACGACTCCATGCCGCCACCTGCATGTGC
GCAGCTACTGCCGACTGGCCCCATCAGCCAACAAGACCTCGCTTCATCTCAAACGCCGGCGAGGGAG
AGGCAACAGCACCCGCCACTGTGCCCTTCCCTCGACATCAAGACCTCATCGCCACCCACCATGGCT
TCATCTTCCCTGGCGTCTCTCTGCTGGCTGCTGTTCTCTGGAGCCGGCAAGGGCAACACAA
AGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCACGCCGGCAAGT
TCAACATGAAGATGATATGAGGCCGGGGCGGGGGAGGGACCCCGGGCGGCCGGCAGGGGAAGGGCTGGT
CGCCACCTGCTCACTCTCCAGTCCTCCACCTCCCTACCCCTACACACGTTCTTTCTCCCTCCGCC
TCCGTCCTCTGCTGCCCGGCCAGCCCTCACCACCTGCCCTCTTCTACCGAGGACCTCAGAACGCCAGACCTGG
GGACCCACCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCATAAAT
TCAATAAAAGTTACGAACTTCTCTGTAACCTGGTTCAATAATTATGGATTTATGAAAACCTGAAATAA
TAAAAAGAGAAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 324

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCFVAVPEGIPTETRL
LDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTLGLRSNRKLIPLGVFTGLSNLTQDI
SENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFGSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLHL
NINAIRDYSFKRLYRLKVLEISHWPYLDTTPNCIYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMILHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLETLILDSPNPLACDC
RLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFDGHTVQFVCRADG
DPPPAILWLSPRKHLVSAKSNGLTVFPDGTLERVRYAQVQDNGTYLCIAANAGGNDSPAHLHVRSYSPDWPHQP
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCVLFLWSRGKNTKHNLIEIEYVPR
KSDAGISSADAPRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCACCGCGTCCGCCACCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGAGAAGAGGCAGGAGCTGGAAAGAGAGAGGGAGGGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGTTAGGAACCAAGAGTAGCCCTGTGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAGAGCAGAGGAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTGAAGGGCGGATCTCAGTCCTGGCTGCTT
TGGCATTGGGAACTGGACTCCCTGTGGGAGGGAGGAAAGCTGGAAGTCCTGGAGGGAC
AGGGTCCCAGAAGGAGGGACAGAGGAGCTGAGAGAGGGGCAGGGCGTTGGCAGGGTCC
CTCGGAGGCCTCGGGG**AT**GGGGCTGCAGCTCGTCTGAGCGCCCTCGAGCGCTGGTACTC
TGGGCTGCACTGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAAACTCGTGCCAGGGCCTCCTTCTGGGGCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGTT
CTTATGACCCCTTCTGCCCTCATTAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGAACC
TTGTACAACACCGGCCGACATGTCTCCTGCCTGCACCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTACAGCCACCGACTCAGTGAAC TGCGGCTGCTGTTGGAGCTCGCAG
GGAGCCGGCTCGGAACATCAGATCAACCACCAAGGGCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAACTCTACGGGAATTTCAGCGCTGCCTCCCGGGCCCAATGGCCTGGCATT
CTCAGCCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCCCTAGTCGCCTCCTAACCGC
GACACCATTCACTCGCATCTCCTACAAGAATGATGCCTACTTCTCAAGACCTGAGCCTGGAG
CTCCTGTTCCCTGAATCCTCGGCTTCATCACCTATCAGGGCTCTCAGCACCCGCCCTGC
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCTGCAGCCCTGGCCCACAGGGCACTGAGGGCAACAGGGACCCCGGCACCCCGAG
AGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGATGGTCCCCCATGGTCGCT**TGA**GAC
TCCCCTCGAGGATTGCACCCGCCGTCTAACGCTCCCCACAAGGCGAGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAALGAAAHHGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLY
SHRLSELRLLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN
VASTSNPFLSRLLNRTDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW
ILIDRALNITSLQMHSIRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGAGCCACACCAGGACTGTGTTGAAGGGTGT
TTTTTCTTTAAATGTAATACCTCCTCATCTTCTTACACAGTGTCTGAGAACATTACATTAGATAA
GTAGTACATGGTGGATAACTCTACTTTAGGAGGACTACTCTCTGACAGTCCTAGACTGGTCTTCAACT
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCCCTGGCTTGTGCTGCAAACCCCTTTAGCCCTTCAC
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACCTCTTTCCAACAAGAGGCCAAGGCAAGGCAATTTCATTGATCTGTTCAA
TGTGTCCTTTGGATGTCAGTGCTATTACGAGTTGACATTGCTCAGATTAGGTTGACCTCAGTCCCAACCA
ACATTCCATTGATACTCGAATGCTTGATCTCAAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAG
GACTCACTTCACTTATGGTCTGATCCTGAACAACAAGCTAACGAAGGATTACCCAAAAGCCTTCAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGCCCCACAATCAACTAAGTGAATACCAACTTAACTCTCCAAATCATTAG
CAGAACTCAGAATTCACTGAAAATAAAGTTAAGAAAATACAAAGGACACATTCAAAGGAATGAATGTTTACAG
TTTGGAAATGAGTGCAAACCCCTTGTATAATAATGGGATAGAGCCAGGGCATTGAAAGGGTGTGCGGTGTCC
ATATCAGAATTGCGAGCAGAAACTGACCTCAGTTCTAAAGGCTTACCAACTTTATTGGAGCTTCACTTAG
ATTATAATAAAATTCAACAGTGGAACTTGAGGATTTAAAGGATACAAAGAACTACAAAGGCTGGCCTAGGAA
ACAACAAAATCACAGATATCGAAAATGGAGTCTGCTAACATACCACTGAGAGAAAATACATTGGAAAACA
ATAAACTAAAAAAATCCCTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTCCTCATTCTAATTCAA
TTGCAAGAGTGGGAGTAAATGACTTCTGCAACAGTGCCTAAAGATGAAGAAAATCTTATACAGTGCAATAAGTT
TATTCAACAACCCGGTGAATACTGGGAAATGCAACCTGCAACATTCTGTTGAGCAGAATGAGTGTTC
AGCTTGGAACTTGGATGTAATTAGTAATTGGTAATGTCCTTAAATATAAGATTCAAAATCCCTACAT
TTGGAATACTGAACCTTAAATGGTAGTTATATACAGCAAAATCTTCAAGTGGTAAGTCC
ACTGACTTATTTATGACAAGAAATTCAACGGAATTGCAAAACTATTGATAACATAAGGGTTGAGAGAAAACA
AGCATCTATTGCAAGTTCTTTGCGTACAAATGATCTACATAATCTCATGCTTGACCATTCTTCTTCAT
AACAAAAAGTAAGATATTGGTATTTAACACTTGTATCAAGCACATTAAAGAAACTGTACTGTAAATGG
AATGCTTGACTTAGCAAAATTGCTCTTCATTGCTGTTAGAAAACAGAATTAAACAAAGACAGTAATGTGA
AGAGTGCATTACACTATTCTTATTCTTAGTAACTTGGTAGTACTGTAATATTAAATCATCTAAAGTATGA
TTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGGCCGTCTTATGTTAAAACATAATTCTTAAAG
TAAAGCCTTCAGTAAATGTCATTACCAACTTGATAAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATAT
GCTTTTTTTTAAATTATTACCTGATTTAAAATCTCTGAAAAACGTGTAGTGTTCATAAAATCTGTAAC
CGCATTAAATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCACTCAA
CTCTAAGGAATATTGGAGATATCCCTTGGAGACCTGCTGGAGAGGCCTGGACACTAACAAATTCTACACC
AAATTGTCTCTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAATTAAACAGACAGAAACCGAAAGCTCTATATAATGCTCAGAGTTATGTATTCTTATTGGCATTCAA
CATATGTTAAATCAGAAAACAGGGAAATTTCATTAAAATATTGGTTGAAAT

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FIGURE 328

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPRS
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGSLANI PRVREIHLENNKLKKIPSGLPELKYLQI
IFLHSNSIARGVNDFCPTVPKMKSLSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:**Signal sequence.**

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGTGT
TTGCCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCAGCAGCCTGCT
GAAGTTGAAATGGTGCAGGTCGTGTTCGACACGGGGCTGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTCAGTTGA
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCTCAATACCA
TGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATGCAGCAAAT
GTTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTCTTCACCAAC
CTTCAACCCACAGGAGGTCTTATTGCTTCCACTAACATTTCGGAATCTGGAGTCCACCCG
TTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCATCCACACTGATGA
AGCAGATTCAAGTCTGTATCCAACCTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACAG
AGGCCGGAGGAGCTGCCTCTTACAGCCAGGAATCTCAGAGGATTGAAAAGGTGAAGGA
CAGGATGGCATTGACAGTAGTGATAAAGTGGACTTCTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTGCACGGATGATCGAAC
GAGAGCTGTGGACACATCCTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTCAGATGGC
AGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCTGGGGATTTGACCACAAATGCCACCGTTGCTGTTGACCTGACCATGGAAC
TTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGTTCTGAATGCCATGTCAGTTA
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATTAAAATAAGTGCCTTATACAATG

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FIGURE 330

MITGVFSMRLWTPGVVLTSILAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQ
PGISEDLKKVKDRMGIDSSDKVDFIILDNVAEQAHNLSCPMLKRFARMIEQRAVDTSLYILPKEDRESIQMA
VGPFLHILESNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTCCGGCTCCGGATGGCACATGTGGGATCCCAGTCTTGGCTACAACTTTCCCTTC
AACAAAGTTCTAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTTGTGCTGGAGAAGAAAGGGCTGAGGGCAG
AGCAGGGCACTCTCACTCAGGGTACCAGCTCCTGCCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGAGCAGTTGA
CCTGGAGAGGCCCTGGGGAGGGCCTGCCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGATAAG
ACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT
TTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTGAAAATAAAATTTAA
AAAAAGCAAGTATTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGG
GAGAAAGTATGTTAAAATAGAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAAGGGATGGGACC
CTGGGTCAAGGCCAGCCTCTTGCTCCTCCGGAAATTATTTTGGTCTGACCACTCTGCTGTGTTTGAGAA
TCATGTGAGGGCAACCGGGAGGTGGAGCAGATGAGCACACACAGGAGCCGTCCTCACCGCCGCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGGACAGCCGCTCTGTTCTGCTCAGTGGT
TGGGTGCTGCTGGCCCCCCCAGCAGCCGATGCCCTAGTCAGCACCTTCACTCTGAGAATCGTACTGGACC
TTCAACCACCTGACCGTCCACCAAGGGACGGGGCCGCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTGTTACCCGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAGCTGCTCATATTGACTACTCTGAGAAC
CGCCTGCTGGCCTGTGGAGCCTCTACCAAGGGGGCTGCAAGCTGCTGCGGCTGGATGACCTCTCATCCTGGT
GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGCACCATGTACGGGTGATTGTGCG
TCTGAGGGTGGAGGATGGCAAGCTTCTCATGGCACGGCTGTGGATGGAGCAGGATTACTTCCGACCCCTGTCC
AGCCGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGATTTGTCTCCTCT
CTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGTACATCTACATCTACGGCTTGCTAGT
GGGGCTTGTCTACTTCTCACTGTCCAGCCGAGACCCCTGAGGGTGTGCCATCAACTCCGCTGGAGAACCTC
TTCTACACCTCACGCATCGTGGGCTCTGCAAGGATGACCCAAGTCCACTCATACGTGTCCTGCCCTGGC
TGCACCCGGCCGGGTGGAATACCGCCTCTGCAAGGCTGTTACCTGGCAAGCCTGGGACTCACTGGCCAG
GCCCTCAATATCACCAAGCCAGGAGCAGTGTACTCTTGCATCTCTCAAAGGGAGAAGCAGTATCACCA
CCCGATGACTCTGCCCTGTGTGCCCTCCCTATCCGGCCATCAACTGCAAGGAGCCTGAGTCTGC
TACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGAGGACGTCCAGTGCACGAAGGCGCTGTCCCC
ATCGATGATAACTCTGTGGACTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTG
TACACCACCAAGCAGGGACCGATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTGTGGGG
ACTAAGAGTGGCAAGCTGAAAAGGTAAAGAGTCTATGAGTTCAAGATGCTCAATGCCATTACCTCCTCAGCAA
GAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTATTTCTGGGAAACAAAGGTGA
AATGGGGAGGTAAGAAGGGGTTAATTGTGACTTAGCTTAGCTACTTCCAGCCATCAGTCATTGGTAT
GTAAGGAATGCAAGCGTATTCAATATTCCCAAACCTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

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FIGURE 332

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSLYQG
VCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEGKLFIGTAVDGKQDYFPTL
SSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLAQ
AFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQNLELNWLL
GKDVKQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT
KSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGGCACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCTGAT
GCGGGACTTCCCCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTACCA
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG
GGATGCCCTGCGCCTCACCCGGAGCAGATTGACCTCATGCCCGCATGTGTGCCTCCTATT
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTACATGCT
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAA
GGCGTCCACTCCTCTACAACAAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCCTGGCATGATGGTAGACTTATCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGGCTGCCGGGTGTGCAA
CAGTCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAAGAACGGTGGCTGTGAT
GGTGTCTTGTCCATGGGAGTAATAACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACCTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATGGGATTGGAGATTATGA
TGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATACCGGTCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAACACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTGCAGTTGTGGCCACCTT
CCCAGTCCTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCAGTGTAGCAAGC
CACAGACACCCACAAAGTCCCTGTTGTGCAGGCACAAATATTCCTGAAATAATGTTT
GGACATAG

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FIGURE 334

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYQ
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALNDTQ
KLA CLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDSLHVSDA VARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLKK
NGGVVMVSLSMGVIQCNP SANVSTVADHF DHIKAVIGSKFIGIGGDYDGAGKFPOQLEDVSTY
PV LIEELLSRGWSEEEI QGVLRGNLLRVFRQVEKVQEE NWQS PLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPV LAVVATFPVLILWL

Important features:

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 335

CCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCAG
AGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCTCCTGCTGCT
GCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGTTTCTGCCAAAAGA
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAAAGAA
GAAGTGTGAGGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCGGATCAA
ACAGACTCTTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCGGATCAA
AAATGTGACAAGAAGTGTGAGGATACAGTCACCTGGAAGTATTAGTGGCTCCAGCAGTCCATCATG
CCAAAACCTGGAAGAGGATACTGGAACTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG
TGAAGTACCTCTTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG
GAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAAATCCCAGACT
TGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAATGGAACCTGCAATTAA
TACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTCTGTGGATATCG
CAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCATCATAGCAGCCGT
AGTAGTTGTGGCTTAGTGATTCCGTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGG
CTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAG
TGAAAATGTGCAGTGGCTACGCCGTAAATCCCAGCACTTGGAAAGGCCGGCGGGCGGATC
ACGAGGTCAGGAGTTCAGCCAGTCTGGCAATATGGTGAACCCATCTACTAAAATAC
AAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGAGACAGGAGAATC
ACTTGAACCCGGGAGGCGGAGGTGCACTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG
TAACAGAGCAAGATTCCATCTAAAAATAAAATAAAATAAAATAACTGGTTTACCT
TGTAGAATTCTTACAATAATAGCTTGATATT

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FIGURE 336

MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVS
APSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT
WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNIISGIIAAVVVVALVISVCGLGV
CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCAGCCTCGG
CACCTGCAGGTCCGTGCGTCCCAGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGCAA
TGATTTC CCTCCCAGGGCCCTGGTGACCAACTTGCTGCGTTTGTTCTGGGCTGAGTG
CCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGCGG
TGGAGGGAGGGAAAGTGGTGTCCAGCGTGGTACACCTGCACGGGAGGTGTCTCATCCC
AGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAAGAAAAGGAGGATCAGGTGT
TGT CCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCCATGCCCT
CCC GGAAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATCAAAACCTTAGAAGTCA
ATG TACTGGTTCCCTCCAGCTCCATCCTGCCGTCTCCAGGGTGTGCCCATGTGGGGCAA
ACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCATACCAGTGGATCGGC
AGCTTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTGGTCTTAAAGCC
TCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCCACAATGAGGTGGCA
CTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGCAAGTGGTCTGGAG
CTGTTGTGGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGCTGGCCTCTGTACCAACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCGGACCC
TGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCCTGTCACCTCCG
CACGAGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTC
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAA
TATCCCCCATCCCTGGTGGGGTTCTTCTGGCTGAGCCGATGGGTGCTGCGCTGTGA
TGGTGCCTGCCAGAGTCAAGCTGGCTCTGGTATTGATGACCCACCACTATTGGCTAAAG
GATTGGGGTCTCTCCTCTATAAGGGTACCTCTAGCACAGAGGCCTGAGTCATGGAAAG
AGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGAGGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGT
GAGGGGAGAGACTCCAGTCAGTGAGTCTCCAGGGCCCTGATCTGTACCCACCCCTAT
CTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTACTGGGCAGAGGATAGGGAATCTTTATTAAAACATGAAATATGTGTT
GTTTCATTGCAAATTAAAGATAACATAATGTTGTATGAAAAA

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FIGURE 338

MISLGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSSS
QPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLOEKDSGPYSC
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWDR
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCAHNEVGTACQCNVTLEVSTGPGAAVVAG
AVVGTIVGLGILLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPWPKSSDTISKNGTLSSVTS
ARALRPPHGPPRPGALTPTPSLSSQALPSRPLPTTDGAHPQPISPPIPGGVSSSGLSRMGAVPV
MVPAQSQAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 339

GCGAGAACCTTGACGCGACAAACTACGGGACGATTCTGATTGATTTGGCGCTTCGATCCACCCCTCCT
 CCCTTCTCATGGACTTGGGACAAAGCGTCCCAGCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA
 GGACAGCGTCGGAACCATGGCTCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGCGGGTC
 TGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
 AACAGAGGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
 CGTGCACAGAGGGTGTGGATTACACCATTGCTTCAACATTGCTTCTTGCCTGCTATGTACAGTTGTAAT
 CAGGTCAAACAAATAAAAGTCTGTACACAGGACAGAGCAGGGATGGTCAAGGTCAAGGTCAAGTAATTGTA
 ATAAAAACTCCCCCTGAGATGCGGAGCTGTAGAACAGGGTGTCCCAGAGGAGCAGGGATGGTCAAGGTCAAGGTCAAGTAATTGTA
 CGCCCCGGAGTGAATGCAAAATGAATCAGCTGCCAGTCTCCACTACCTTATCATAGTGGTTTAGTCATCATT
 CAGTGACCAACATCCTGGGGATGCTGCCTCTCCATCACTACCTTATCATAGTGGTTTAGTCATCATT
 TAGCTGTGGTTGTGGTTGGCTTCTATGTCAAAGAAATTCAATTCTTACCTCAAAGGCATCTGCTCAGGTGGT
 GAGGAGGTCCCAGACGTGTGCACAGAGCTTCCGGCGGCTCATGCTCTCACAGGACCAACTGGGGCTCGAAAAGCTCT
 ACAATGCCGCAACAGGACATGCAAAGGAAACAATTAGGACCAACTGGGGCTCGAAAAGCTCT
 AGGAGCTGGCAGAGCTAACAGGTGTACTGTAGAGTCGCCAGGGAGCCACAGCGTGTGCTGGAACAGGCAGAAG
 CTGAAGGGTGTCAAGAGGAGGAGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTGCTGG
 ATGCTCGGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTAGGACCAACTGGGGCTCGAAAAGCTCT
 TTTATGAAGAAGATGAGGAGCAGGCTCTGCTACGTCCTGCCTGTGAAGAATCTCTTCAGGAAACCAGAGCTCCCT
 CATTACCTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAAACT
 CTACTATCCAATATGGGGAGCTTACCAATGGCTCTAGAAACTTGTAAACGCACTTGGAGTAATTGTAAT
 ACTGCGTGTGATAAGCAAACGGGAGAAATTATATCAGATTCTGGCTGATAGTTACGATTGTGATTAAAG
 GTCGTTTAGGCCACATGCGTGGCTCATGCCGTAAATCCCAGCACTTGTAGGCTGAGGCAGGTGGATTGCTT
 GAGCTCGGAGTTGAGACCAGCCTCATCAACACAGTGAACACTCCATCTCAATTAAAAGAAAAAGGGGGGGGG
 TAGGATGTCATTCTTGCAAGTCTTCATCATGAGACAAGTCTTTCTGCTCTTATATTGCAAGCTCCATCT
 CTACTGGTGTGCAATTAGACATCTAACTACAGATGCCGACAGCCACAATGCTTGCCTTATAGTTTA
 ACTTTAGAAGCAGGATTATCTGTTACCTGTATTTCAGTTCCGGATATTGTAATGATGAGATTATC
 AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTCTGACTTAGAGTTGAGCTTAAAGATA
 GGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTATATTGCTACTACTGTAGGCTGTACATCT
 TTCCGATTGGTATAATGATGTAACATGGAAAACATTAGGAAATGCACTTATTAGGCTGTTACATGGGG
 CCTGGATACAAATCAGCAGTCAAAATGACTAAAATATAACTAGTGACGGAGGGAGAAATCTCCCTCTG
 AGGCACTTACTGCATTCCAGTTCTCCCTGCGCCCTGAGACTGGACCAAGGGTTGATGGCTGGCAGCTCTCA
 AGGGCAGCTGTCTTACTTGTAAATTAGAGGTATATAGCCATATTATTTATAAATAAATATTATTATT
 ATTATAAAGTAGATGTTACATATGCCAGGATTGAGGGCTGGTATCTTGGGAAGGCCATGTGCTGG
 GTCGTCGGACAGTCATGGGACTGCATCTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAGTAG
 ATCCGAGACTGCGAAGAGCTCTTCAAGGCCATTACAGTTGAACGTTAGTGAATCTTGAGGCTCATTGG
 CTCAGGGCAGAGCAGGTGTTATCTGCCCGCATCTGCCATGGCATCAAGAGGGAGAGTGGACGGTGTCTGG
 AATGGTGTGAATGGTTGCCGACTCAGGCATGGATGGCCCTCTCGCTCTGGTGTGACTGAGTCCCT
 GGGATGCCCTTGTAGGGCAGAGATTCTGAGCTGCGTTTAGGGTACAGATTCCGTTGAGGAGCTGGCC
 CTGTAAGCATCTGACTCATCTCAGAGATATCAATTCTAAACACTGTGACAACGGGATCTAAAATGGCTGACACA
 TTGTCCTTGTGTCAGCTTCATTATTAAACCTCAGTAATGTTAGCTTCTTCCAGCAAACACT
 TCTCCACAGTAGCCCTGCTGGTAGGATAATTACGGATATAGTCATTAGGGGTTTCAGTCCTTCCATCT
 AAGGCATTGTGTGTTGGAGTTAGGGAGGGATGGCCTTCCGGTCTTCGCACTTCCATCTCCACTTC
 TGGCGTCCCACACCTTGTCCCGTGCACCTCTGGATGACACAGGGTGTGCTGCCTCCTAGTCCTTGCCTTG
 GGCCTCTGTGCAGGAGACTGGTCTCAAAGCTCAGAGAGGCCAGTCGGTCCAGCTCTTGTCCCTC
 AGAGGCCTTCTGAAAGATGCATCTAGACTACCAGCCTTATCAGTGTAAAGCTTATCCTTAACATAAGCTTC
 CTGACACATGAAATTGTTGGGGTTTTGGCGTTGGTTGATTGTTAGGTTGCTTATACCCGGGCAAAT
 AGCACATAACACCTGGTATATGAAACTCATATGTTATGACCAAAATAATGAAACCTCATRTTAAAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVQQTVAPQQQR
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNLLPSCLLCTVCKSGQTNKSSCTTRDTCQCCEKGSFQDKN
SPEMCRTCRTGCPRGMVKVSNCPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIIILAV
VVVGFSRKFFISYLGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL
AELTGVTVESPEEPQRLLQEAEAGCQRRLLLPVNDAADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE
EDEAGSATSCL

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 341

GCCTCTGAATTGTTGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTCTGCCAGATTGGCTTCAGCTCCTGTTAATTCTGGCTTGGCCAGG
CAGTCCAATTCAAGAAATATGTCTTCTCCAATTCTGGGCTTAGATAAGGCGCCTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCAGCGA
CCACTGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGCGTCCGGGAATGTACTTC
GCTTCTCCCAGACCAAGGTTCTTACCCAAAGAAAATTCCCAAGCTTCTCCTGCC
TGCAGAAGCTCCTCTACTTAAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCC
AGCTGGGCCTGGACTTGGGCCAATTCTACTATAACCTGGGACCAGAGCTGGAACCTGGCTC
TGTTCTGGTTCAGGAGCCTCATGTGTGGGCCAGACCACCCCTAACGCCAGGTAAAATGTTG
ATTGGAATGACAACCCCCGGAAAAATTCCGGTTATTCCCTGGAGATACTGGTCAAAGAAGATA
GAGACTCAGGGGTGAATTTCAGCCTGAAGACACCTGTGCCAGACTAACGATGCTCCCTCATG
CTTCCCTGCTGGTGGTACTCTCAACCCCTGATCAGTGCCACCCCTCTGGAAAAGGAGAGCAG
CCATCCCTGCCCCAAGCTTCTGTAAGAACCTTGCCACCGTACCCAGCTATTCAACT
TCCGGGACCTGGTTGGCACAAGTGGATCATTGCCCAAGGGTTATGGCAAATTACTGCC
ATGGAGAGTGTCCCTCTCACTGACCATCTCTCAACAGCTCCAATTATGCTTATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTATCCCCACCAAGCTGTCTC
CCATTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTCTTAGGG
TAAATCTTTAATAAAACTACCTATCTGGTTATGACCACTTAGATCGAAATGTC

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FIGURE 342

MLRFLPDLA
FSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAAT
TGVSRDLCYVKE
LGVRGNVLRF
LPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LG
LDLGPNSYYNLGPE
LELALFLVQE
PHVGQTTPKPGKMF
VLRSPWPQGA
VFNLLDVAKD
WNDNPRKNFGLF
LEILVKEDRD
SGVNFQPEDTC
ARLRC
SLHASLLV
VTLNPDQCHPSRK
RRAA
IPV
PKLSCKNLCHR
HQLFINFR
DLGWHK
WIIAPKG
FMANYCHGECP
FSLTISLN
SSNYAFM
QALMH
HAVDPEIPQAVC
IPTKLSP
ISM
LYQDN
NDNV
ILRH
YEDMV
VDECGCG

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 343

CCACCGCGTCCGGCCTCTCTGGACTTGCAATTCCATTCTTTGATGACAAACTGACTTTTTATTCT
TTTTTCATCTGGCCAGCTGGGATCCTAGGCCGCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTCTCCTCCCTGACATTGCATTGCTAGTGGTGTGTTGGGAGGGAGACCACGTGG
GCTCAGTGCCTGACTATCTGCTAGTACATCGAAGTCTTGTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGTATCCTGGCCCTGCTCCTGCTGATAGTGTGCTGTCTTACTTCAAATACACAAAC
GCGCTAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAATCACAAACCCAGACAAGGTGTGGTGGGCAAG
AACAGCCAGGCCAAACCATGCCACGGAGTCTGTGCTGCCAGTGTGAAGGATATAGAATGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCTTCCAGGAAGGGAGTTGGGGAGAGAACCCTACTGTGGGAATGCTGATAAAACCAGTC
CACAGCTGCTATTCTCACACAAATCTACCCCTTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGCGTCTTAAGGCTGCCAGCGCCTGCCAAA**ATGGAGCTTGTA**
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTGTTGGCGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCCAATATGGCAGAGACCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAGTCTTGACGGAACCTCCAGCAATGGGCCCTGCTAGGG
CAAGTCTGCAAGTAAAAGACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTGTCTTACTACTCTCTCCTAAACATCTTCTATTC
GGCGGTTACCTGGATACCTTGGAGGATCCTCAGGCCAATTACCCAAAGCCGATCTGGCTGAGCTGGCTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCATAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTCGAATCGTCAAAACTCTGTGACTGTCGTGTTGCTACAGATTATGCCAATCT
TACCGGGATTTCCTGCTTCAACACCTCAATTATGCAAGAAACATCAACACTACATCTTAACTTGCTCTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTTAACTCTAATGGGATAACTTGCAACTAAA
GACCCAACTGCAAGACAAAATTATCAAATGTTGGAATTTCCTGCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATATAATCACCTTCTGCACTCCTCAACTCTGAAGTGTGATCACC
CGTCAGAAACAACCTCAGATTGTGAAGTGTGAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACACCAGCATGGCTTTGAATCCAATTCA
TTGAAAAGACTATACTGAAATCACCATATTATGGAATTGAAACCAAACCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTGTCTGATACTGTAGAGCCTCTCCACCTGACTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACCTGTAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTCTGTGATCTGCAAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCACTCGCTGCAATCAAGGTTGTCTCCAGAAGCAACGAGACATTCTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTAGGATTTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCACTGTTCCATGGTTCTAGCTCG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGCAGACTACAAATACAGAAGCTG
CAGAACTATTAACTAACAGGCTCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGCACACAGGCCTGCATGTAAAAAAA

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FIGURE 344

MELVRRRLMPLTLLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE
RPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSTLTFO
IVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD
YKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLDY
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV
VEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNSTVEIIYI
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVFLDT
CRASPTSDFAFPYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD
SSDHQSRCNQGCVSRSKRDISSYWKTDIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Important features:

Signal sequence:
amino acids 1-24

Transmembrane domain:
amino acids 571-586

N-glycosylation site.
amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.
amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.
amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.
amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 7-18

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FIGURE 345

TGGGGGCCCCCCCAGGCTCGCGCGTGGAGCGAAGCAGCATGGGCAGTCGGTGC CGCCTGGCCCTGGCGGTGCTCT
GCCCTTGCTGTGTCAGGCTGGAGCTCTGGGGTGTGCAACTGAAGCTGCAGGAGTTCGTCACAAAGAAGGGGT
GCTGGGGAACCGCAATTGCTGCCGCGGGGGCACCAGCCGTGCGCTTGCGGACCTTCTCCCGCGTGTG
CCTCAAGCACTACCAGGCCAGCGTGTCCCCCGAGCGCCCTGCACCTACGGCAGCGCCGTACCCCCGTGCTGG
CGTCGACTCCTCAGTCTGCCGACGGCGGGGCGCCACTCCCGTTCAGCAACCCATCGCCTCCCTTCGG
CTTCACCTGGCGGGCACCTCTCTGATTATTGAAGCTCTCACACAGATTCTCCTGATGACCTCGCAACAGA
AAACCCAGAAAAGACTCATAGCCGCCTGGCACCCAGGGCACCTGACGGTGGCGAGGAGTGGTCCAGGACCT
GCACAGCAGCGGCCACGGACCTCAAGTACTCCTACCGCTTGTGTGACGAACACTACTACGGAGAGGGCTG
CTCCGTTTCTGCCGCTCCCAGGACATGCCCTCGGCCACTTCACCTGTGGGGAGCGTGGGAGAAAGTGTGCAA
CCCTGGCTGAAAGGGCCACTGACAGAGCCGATCGCTGCTGGATGTGAGGAGCATGGATTTGTGAA
CAAACCAAGGGGAATGCAAGTGCAGAGTGGCTGGCAGGGCGGTACTGTGACGGAGTGTATCCGCTATCCAGGCTG
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCACACTGCCAGGAAGGCTGGGGGGCCTTTCTGCAACAGGA
CCTGAACTACTGCACACACATAAGGCCCTGCAAGAATGGAGGCCACTGCACCAACACGGGCCAGGGAGCTACAC
TTGCTCTGCCGCTGGGACACAGGTTGCCACTTGTGAGCTGGGATTGACGAGTGTGACCCCAGGCTTGAA
GAACGGAGGGAGCTCACGGGATCTCGAGAACAGCTACTCCTGTACCTGCCACCCGGCTCTACGGAAAATCTG
TGAATTGAGTGCATGACCTGTGCGGAGGCCCTTGCTTAACGGGGTGTGCTCAGACAGCCCCGATGGAGG
GTACAGCTGCCGCTCCCCGTGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCAGCTCTCAC
CTGTTCTAATGGTCCAAGTGTGGAACCTCGGTGATGCCCTACCTGTGCCGTGCCAGGCCGGCTCTGGGGAG
GCACTGTGACGACAACGTGGACGACTGCCCTCCTCCCGTGCGCCAACGGGGCACCTGCCGGATGGCGTGA
CGACTTCTCCTGCACCTGCCGCCCTGGTACACGGGAGGAACGTGAGTCCCCGTGACAGGTGCGAGCACGC
ACCCGCCACAATGGGCCACCTGCCACGAGAGGGGCCACCGTATGTTGCGAGTGTGCCAGGGTACGGGG
TCCCAACTGCCAGTCTCTGCTCCCCGAGCTGCCAGGGGCCAGGGTGGACCTCACTGAGAAGCTAGAGGG
CCAGGGGGGCCATTCCCTGGGTGGCCGTGCGCCGGGTATCCTGTCCTCATGCTGCTGCTGGCTGTG
CGCTGTGGTGGCTCGTCCGGCTGAGGCTGAGAACGACCCGCCAGCCACCCCTGCCGGGGAGACGGA
GACCATGAACAAACCTGCCAAGTGCAGCGTGAGAAGGACATCTAGTCAGCATCGGGGCCACGAGATCAA
GAACACCAACAAGAAGCGGACTTCCACGGGACCAAGCGCCGACAAGAATGGCTCAAGGCCGCTACCCAGC
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGAAGCACCCGCTCAGGGACGCGCACAGCAAGCGTGA
CAAGTGCAGCCCCAGGGCTCTCAGGGGAGGAAGGGGACCCGACCAACTCAGGGTGGAGAACGATCTG
AAGAAAAGGCCGACTCGGGCTGTTCAACTCAAAAGACACCAAGTACCGAGTGGTGTACGTCATATCCGAGGA
GAAGGATGAGTGCCTAGCAACTGAGGTGAAAATGGAGTGGCAAGACTCCCGTTCTTCTTAA
AGTAAAATTCCAAGGATATATGCCCAACGAATGCTGCTGAAGAGGGAGGGAGGCTCGGACTGCTGAGAA
ACCGAGGTTCAAGACCGAGCAGGTTCTCCTCGAGGCTCTCGACGCCCTGCCAGCGCACAGCAAGCGTGA
TGGCCACTGCCCTCCGTGACGTGCCGTGCACTATGGACAGTGTCTTAAAGAGAAATATATTTAA
GAACCTGAACTACGCTAAGAACGATGCACCTGCCAGGTATATTGGATTCTTATGAGCCAGTCTTCTTGT
ATTAGAAACACAAACACTGCCCTTATTGTCCTTTTGATACGAAGATGTGCTTTCTAGATGGAAAAGATGTG
GTTATTTTTGGATTGTAAGGAAATATTTCATGATATCTGAAAGCTGAGTATTGTGATGTTGCTT
TAATTTAAATTGGTAAATATGACAAAGGACTCGGGTCTATGTGACTATATTTTTGTATATAAATGTAT
TTATGGAAATTGTGCAAATGTTATTGAGTTTTACTGTTGTTAATGAAGAAATTCTTTTAAAATATT
TTCCAAAATAAATTATGAATGACAAAAA
AAAAAAAA

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FIGURE 346

MGSRCALALAVSALLCQVWSSGVFELKLQE VNKKGLGNRNCRGAGPPPACRTFFRVC
LKHYQASVSPEPPCTYGSAVTPVLGVDSFLPDGGGADSAFSNPIRFPGFTWPGTFSLIIEA
LHTDSPDDLATENPERLISRLATQRHLTVEEWSQDLHSSGRDLKYSYRFVCDEHYYGEGCS
VFCPRRDDAFGHFTCGERGEKVCNPWKPYCTEPICLPGCDEQHGFCDKPGECRKCRVGWQGR
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGFLFCNQDLNYCTHHPKCKNGATCTNTGQGSYTCS
CRPGYTGATCELGIDECDPSPCKNGSCTLENSYSCTCPPGFYKGKICELSAMTCADGPCFNG
GRCSDSPDGGYSCRPCVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
DNVDDCASSPCANGTCRDGVNDFSCTCPGYTGRNCSAPVRCEHAPCHNGATCERGHRYV
CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWAVCAGVILVLMLLLGA
CVRLRIQKHRRPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKADFHDHSADKN
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSGEEKGTPTLRGGEASERKPD
SGCSTS KDTKYQSVYVI SEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185;252-261

N-myristoylation sites:Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;
676-682;683-689;695-701**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;
467-479;505-517

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FIGURE 347

CCACCGCGTCCGACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAACA
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTAGGCTGCCAGGCCAGGCCAG
GGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGCGCCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCAACCCTGCTCAGCAGACTCTACTTTGGGAGAAGAGAGGCC
TTCGAGATAATCGAATTAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATTTCACTATGCCGTGCGAAGTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTTATAATCTT
CATTACGGAAAAAGACACAGCCACCCCTAACTGTCACTGCTTCTGGGAGCAAGCCTGCAGGCC
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAAACCTTCACTGTCAAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG
GGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCCCTCCCCATCCTCGT
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGCAGCTACA
AGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCTCCTCCAGCACCTACC
ACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTCATCATGCTCATCTTCC
TTGCCACTACTGATCCGGACAAAGGAACCTACCTGACACATGAGGCAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGCCATCATCAATGCAGAAGCGGGAGTCAGGAGGGAGCACA
AGAAGGAATATTCATCTAGAGGCGCTGCCACTTCCTGCGCCCCCAGGGGCCGTGGGG
ACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCGCTT
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTGGGTGGGTTGCTCAGCCCTTCCGTGGCTT
TTGGAATGGGGAGGGAGGGAGGGCGGGGGAGGGAGGGTTGCTCAGCCCTTCCGTGGCTT
CTCTGCATTGGGTTATTATTATTGTAAACAATCCAAATCAAATCTGTCTCCAGGCTGG
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACAAACAAAAACA

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FIGURE 348

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLYFGEKRALRDNRIQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLVTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFT
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

FIGURE 349

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGACTAACAGAACCCCATTCCAGTCATTTGATTTGCTTTATTTTTTTCTTTTCTT
TTTCCCACACATTGTATTTATTCCTGACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGG
CTTTTCTGAAGTCTTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA
GTGTGTGCCGTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTGCCTCTGGGATCCCG
AGGGCGTAACCGTACTCTACCTCCACAACAACAAATTATAATGCTGGATTCCTGCAGAACTGCACAATGTAC
AGTCGGTGCACACGGTCTACCTGTATGCAACCAACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAG
TTCTCCATTGCAAGAAAACAATTACAGACCATTACGGGCTGCTTGGCCCAGCTCTGAAGGCTGAAGAG
TGCACCTGGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGGCCTCCGGAGGCTATTAGCCTCAAAT
TGTTGTTTTGTCTAAGAACCTGAGCAGTGTGCCTGTTGGCTCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAATCTCACCGAGCTTGGAGCGTCTATTGTGGACG
GGAACCTCCTGACCAACAAGGGTATGCCGAGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTG
TACGTAATTGCTGTCCCACCCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACC
AGATAAACACACATTCTTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGC GGATGCTGACTCAAGGGTTTTGATAATCTCTAACCTGAAGCAGCTCACTGCTCGGAATAACCCCTGGT
TTTGTGACTGCACTTAAATGGGTACAGAACGGCTCAAATATATCCCTCATCTCTCAACGTGCGGGGTTCA
TGTGCCAAGGTCTGAACAAGTCCGGGGATGCCGTAGGGAAATTAAATATGAATCTTGTCTGTCCCACCA
CGACCCCCGGCCTGCCCTCTTCAACCCAGCCCCAAGTACAGCTCTCCGACCCTCAGCCTCCACCCCTCTCA
TTCCAAACCTAGCAGAACGCTACACGCCAACCTTCTGAACGGATCCAGCCTCTATCCATTGTAATGATACTCCATT
GCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCCTCTATCCATTGTAATGATACTCCATT
AAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATACAAACTCACATGGTGAAATGGGCCACAGTTAGTAG
GGGGCATCGTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTACTTAGAGCCCCGATCCA
CCTATCGGATTGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTCAGAGGCCA
CCACCCATGCCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCCACAGCATGG
GCTCCCCCTTCTGCTGGCGGCTTGATCGGGGGCGCGTGTGATATTGCTGGTGTGCTAGCGTCTTT
GCTGGCATATGCACAAAAGGGCGCTACACCTCCAGAACGGAAATACAACCGGGCGCGGAAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCTGGAGATGACAGAACCGAGTTTCAGATCGTCTCCTAA
ATAACGATCAACTCCTAAAGGAGATTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAAATTACACAG
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGCACTGCCATACG**TGAC**AGC
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTCACATAAGACACGCAG
ATTACATTGATAATGTTACACAGATGCATTGCAATTGAAACTCTGTAATTACGGGTACTATATAA
TGGGATTTAAAAGTGCTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTTGCTTTAA
TCTT

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FIGURE 350

MGLQTTKWPSPHGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIPE
GTVVLYLHNNQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR
AALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSSVPVGLPVDLQELRVDE
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDLPGT
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLNSNLKQLTARNNPWFC
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELNMNILLSCPTTPGLPLFTPAPSTAS
PTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDRGRERVTTPPISERIQLSIHFVNNTSIVQSW
LSLFTVMAYKLTWVKMGSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPILDNYRAV
EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVLLSVFCWHMH
KKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNDQLLKGDFRLQPIYTP
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 351

AGCCGACGCTGCTCAAGCTGCAACTCTTGTGCAGTTGGCAGTTCTTTCGGTTCCCTCCTGCTGTTGGGGCA
 TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGAGGGAGGAGCGCGCACCGGACCGC
 GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTGTGCCGGGCCCGAGCGCGCCGGCTGGAGCTTCGGGTAGA
 GACCTAGGCCCTGGACCGCGATGAGGCCGCCAGCCTCCGTGCCGCCGGCTGGAGCTTCGGGTAGCGCTGTGC
 GCGGTGCTGGGGCGCTGGCGCTGGCGCTGGACAGCGCGGTGCGGGAACTCGGGCAGGGCTGGAGCTTCGGGTAGCGCC
 GAGCGCCCATGCCCACTACCTGCGCTGCCCTGGGAGCTGCTGGAGCTGAGTCATAAGCGGCTAGCGCTT
 CCCGAGCCACTCCCCTGGTCGCTGGCTGGAGCTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
 ATGAGCCACCTCAAAGCCTCGAGAAGTGAAGACTGAAACAACATGAATTGGAGACCATTCAAATCTGGGACCA
 GTCTCGGCAAATATTACACTCTCTCCTGGCTGAAACAGGATTGTTGAAATACTCCTGAAACATCTGAAAGAG
 TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATTCCAGGCCATACAG
 CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAATTGGCCAACACA
 CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTAAACTGCCCAACTGCAA
 CATCTGAATTGAACCGAAACAAGATTAAGGATGAGATGGACTGACATTCCAAGGCCCTGGTGTCTGAAGTCT
 CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGGCTGAGCAACATGAAATTGG
 CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCTGAGGAACCTCAT
 CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
 ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCTGGCTAAGCTTACTAAATACACTGCACATTGGG
 AAACAACAGAGTCAGCTACATGCTGATGTTGCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC
 AATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGGCTGACAAACTGAGGGCACTGATAACTC
 CAAGGAAATCGGATCGTTCTATTACTAAAAAGCCTTACTGGTGTGGATGCTGAGCTAGCTGAGT
 GACAACGCAATCATGCTTACAAGGCAATGCTTACAAATGAAGAAACTGCAACAATTGCAATTAAATACA
 TCAAGGCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGGGAAACAAACTTCAAGAGCTTGT
 AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGTGTGATGCCAGATGGCTTGT
 GATGATTTCACCCAAACCCCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTT
 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGAACACTGATGAT
 GCTGAAATGAAAATTATGACACACCTCAGGCCCCAAGGTGGCAGGTGATGGAGTATACCACCATCCTGGCTG
 CGCAGGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTATCTCAACTTGGTTCATCCTACTCTGTC
 AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCAACAGACCCCCATGGATCTCACCATCCAGCTGGGCC
 ATGGCACGCTTGGAGTGTGCTGTGGGACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
 TTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGGATGACGTGTTCTTATGTTGAGTGTGAAGATA
 GAGGACATTGGGTATACAGCTGACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
 CTAGAAACACCATCATTGGCCACTGTTGGACCGAAGTGTAAACAAGGGAGAACAGCCGCTACAGTGC
 ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACGGACAAAGATGATAGCCATTGGTGTAAAGGAGAC
 TTTTGCAGCAGGCAATCAGCTCTGATTATGTTGAGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG
 ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCAGCTGAGGAGCTGGGAAACCTCCACCTCGGACTCCCT
 CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
 GTGGTGGGACGTCAGTGTGTTGGTGTATCATATAACACACAAGGGAGGAATGAAGATTGCAAGGAG
 AACACAGATGAGACCAACTTGGCAGCAGATATTCTCAGTTATGTCATCTCAGGGAAACGTTAGCTGACAGGAG
 GATGGTACGTGCTTCAGAAAAGGCCACCCAGTTGTACATCTCAGGTGCTGGATTTCATACCA
 CAACATGACAGTGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGCCACAGATCTGTC
 CTTTGCCATTGGATCCACAGGCCATTGTTGAAGGGAAATGTGTATGGCTCAGATCTTGTAAACA
 TATCATACAGGTGCACTGACCCAGAACAGTTAATGGACCAACTGAGCCAGTTACATAAAAGAAAAAG
 GAGTGCCTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTTCAGTAATATATGTCAGGCTTCACAT
 GTGAGGAAGCTACTAACACTAGTTACTCTCACATGAAGGACCTGGAAATGAAAATCTGTCATAACAGTCC
 TCTTAGATTTAGTGCACGAGGCCAGCGTGGTTGCCTCGAGTAATTCTTCATGGTACCTTGGAAAAA
 GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTAT
 TTGAAAGCTCATTCTCCCAGACTTGGACTCTGGTCAGAGGAAGATGGGAAAGAACAGGACAGATTTCAAGGAA
 GAAAATCACATTGTACCTTAAACAGACTTTAGAAAAGACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
 ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACACTCAAGTGAACCTTATTTAAAGAGAGAAT
 CTTATGTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTTATACAGATGAACCAAATAC
 AAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTATTGACTTGGAC
 TTTATGAAAAAGTATCTACGTAATTAAATGATATAACATGATTATTTATGATTATTTATAATGCCAGA
 TTTCTTTATGAAAATGAGTTACTAAGCATTAAATAACCTGCCATTGTAACCAATTAAATAGAAGGTT
 ACTTCATTATATTGCACTTAAATGTCATTGAAAGAAAAAAAAAAAAAA

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FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGEIQLQPSGVAERPCPTTCRCLGDLDCSRKRIARLPEPLPSW
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAINTLLSLAGNRIVEILPEHLKEFQSLETL
DLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNIALNTLLVLKLNRRNISAIAPPKMFKLQLQHLELRN
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEIQLDHNNITEITKGWLGYGLMLQELHLSQNAIN
RISPDAWEFCQKLSLELDLTFNHLSRIDDSSLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLSDLKNNEISWTI
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHNTSSLCDC
QLKWLQPQWAENNFQSFVNASCAPQLLKGRSIFAVSPDGVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS
SDSPMTFAWKKDNEELLHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
CTAQNSAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHFFAAGNQ
LLIIVDSDVSDAGKYTCEMSNTLGTERGNVRSLSVIPTPTCDSPQMTAPSLLDDGWATGVVIIAVVCCVVGTSLV
WVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQDGYSSESQSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLKGNVYGSDFETYHTGCSPDPRTVLMHDYEPSYIKKKECYPCH
PSEESCRFSNISWPSHVRKLLNTSYSNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHL
DAYSSFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYLDLT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

Casein kinase II phosphorylation site.amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

N-myristoylation site.amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTTCTGGCTCGGACATTGG
AGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTGTTACTTGATGAGATCGGGATGA
ATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTGCTGGAGACGTCTTTGTTGCCGCTGGAAACGTTAC
AGGGGACGTTGCAAAGAGAAGATCTGTCCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAA
GGGCTTCACAAGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTCTGCATGGCAATTCCCT
CACTCGACTTTCCCTAAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGGAAAACAATGGCTTGCA
TGAAATCGTTCGGGGGCTTCTGGGCTGCAGCTGGTAAAAGGCTGCACATCAACAACAAGATCAAGTC
TTTCGAAAGCAGACTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATAT
AGACCCGGGGCCTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACC
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCCCTATGA
GGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCGGACTGACCTGTGATCT
GCTCTCCCTGAAAAGAATGGCTGGAAAACATTCCAAGAATGCCCTGATGCCCGAGTGGCTGCGAAGCCCCAC
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGCTTGAACCGAGTGGATTCTAG
TCTCCCGCGCCCCCTGCCAAGAAGAGACCTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCA
AGAGGATCATGCCACACCAGGGTCTGCTCAAACCGAGGTACAAAGATCCAGGCAACTGGCAGATCAAATCAG
ACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAACAGTTACCCGCCCTGGGCTG
CAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTGGCTGATTT
GAAGCCAAGCTCTCTAACGTGCAAGGAGCTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCATT
TGTGGATTACAAGAACCTCATTCTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAA
GAACCTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGAGAAATTGGGG
GCTGAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCGGGACTTTCAATGCCAT
GCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGGCTC
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCGGTGGCAGGGTGTGGACCGAGTTAACCTC
CATCATCCAGATAGACCTCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCCTCAAGCAGTGGCAGA
ACGTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTTTAGAAAGGATTTCAT
GCTCCTCTCAAATGACGAGATCTGCCCTCAGCTGTAGGATCTGCCACGTTAACCTGCACAGTAAAAAA
CAGCACTGGTTGGCGAGACCGGGACGCACTCCAACCTACCTAGACACCAGCAGGGTGTCCATCTGGTGT
GGTCCCGGACTGCTGGTTGTACCTCCGCCCTCACCGTGGTGGCATGCTCGTTATCCTGAGGAA
CCGAAAGCGGTCCAAGAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAATTCCCTACAGACAGTGTGACTC
TTCCTACTGGCACAATGGGCTTACAACGAGATGGGCCACAGAGTGTATGACTGTGGCTCTACTCGCTCTC
AGACTAAGACCCCAACCCAAATAGGGAGGGCAGAGGGAGGGGATACATCCTTCCCACCGCAGGCACCCGGG
GGCTGGAGGGCGTGTACCCAAATCCCCGCCATCAGCCTGGATGGGATAAGTAGATAAAACTGTGAGCTC
GCACAACCGAAAGGGCCTGACCCCTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGA
GCGCAGCCAGCTCGCTTTGCTGAGAGCCCTTGTACAGAAAGCCCAGCACGACCCGCTGGAGAAACTGACA
GTGCCCTGCCCTCGGCCCCGGGCTGTGGGTTGGATGCCCGGTTCTATACATATACATATCCACATC
TATATAGAGAGATAGATATCTATTTCCTGTGGATTAGCCCCGTGATGGCTCCCTGTGGCTACGCAGGGAT
GGGCAGTTGCACGAAGGCATGAATGTATTGTAATAAGTAACCTTGACTCTGAC

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FIGURE 354

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCCEKKGFTSLQRFTA
FLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF
LGDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHLDLRGNRL
KTPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDL
NETTEQDLCPLKNRVDSSLAPPQAETFAPGPLPTPKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPSGLKMNCNNRNVSSLADLKPKLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLEYLNVEYNALQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVIMSDLKCETPVNF
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLL
SAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSYYWHNGPYNADGAHRVYDCGS
LSD

Important features:

Signal sequence:
amino acids 1-15

Transmembrane domain:
amino acids 618-638

N-glycosylation site.
amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 122-126, 646-650

Casein kinase II phosphorylation site.
amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.
amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 337-348

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FIGURE 355

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGCTGCACCGGGCCTG
GCAGCGCTCCGCACACATTCTGTCGCGGCTAAAGGAAACTGTTGGCCGCTGGGCCGCGGGGGATTCTTG
CAGTTGGGGGTCGTGGAGCGAGGGCGAGGGGAAGGGAGGGGAACCGGGTTGGGGAAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCGCTCCTGAGCGGGACAGATCCAAGTTGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGAATGGAGGCCGGCTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCGGGGCGGGCG
CGAACACCCACTGCCGACCGTGTGGCTGCTCGGCCCTGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA
GCGGCAGGCCGGAGGGCTGCATCCTGCGAGGTGGGGCCTCAGCACCGTGCCTGCAGCTGC
CGCTGTGCTCGCCTCTGGCCAGGGCCAGGGCCGGAGGGGCTCCAAAGACCTGCTGTTCTGGTCGCACT
GGAGCCAGGCAGGCTCCACTGCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCCGACCCCG
CGGTCTGAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGCGGTACT
CCAGGCCACCGTGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGT
CAAGTACCAAGTTGAGGTCTTGTGCTCTGCGCCGCCGGGGCCCTCTAACCTGAGCTATCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGACCGAGGTGAGTGCCTGCGCCGGGACAGCTCCC
GATCTCAGTTACTTGCATCGGGACGAATCGGCCTCGCTGGACAAACTCTGGGGGATGTGTTGTCCCTG
CCCCGGGAGGTACCTCCGTGGCAAATGCGCAGAGCTCCCTAACGCTTAGACGACTTGGGAGGCTTGCGCT
CGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTCTGTGACCGAGTGGGAAGGACAGCCGACCC
TGGGGGACCGGGGTGCCACCAGGCCGGCCACTGCAACCAGCCCCGTGCCAGAGAACATGGCAAAT
CAGGGTCGACGAGAAGCTGGAGAGACACCACCTGCTGAACAAGACAATTCAAGTAACATCTATTCTGAGAT
TCCTCGATGGGATCACAGAGCACGATGTCTACCCCTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGGAGCGTGATTCCAAGTTAACCTACGACTTCTGCCACTCCTCAGGCTTCGACTCCTCCTC
TGCGTGGCTTCATATTGTGAGCACAGCAGTAGTACTGTTGGTGTCTGACCATGACAGTACTGGGCTTGT
CAAGCTCTGCTTCACGAAAGCCCCCTTCCAGCCAAGGAAGGAGTCTATGGGCCGGGCTGGAGAGTGA
TCCTGAGCCCGCTGCTTGGCTCCAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCT
GCGGGACAGAGCAGAGGTGCCCTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCAATAGGAAACAGGGGACA
TGGGCACCTCTGTGAAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTACTTGTGAACTGACAA
TTCTGCAAGAAATCCCCCTTCTCTAAATTCCCTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTC
CCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGATGGTATACTGGGGACGGGTAGTGCCTGGGAGAGATATT
TTCTTATGTTATTGGAGAATTGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATAT
AATTACATTAAAAAAATATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTCAAGCTAGGAGTATATTGG
TTCGAAATCCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

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FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGAIST
VRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLESD
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGASN
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPRKESMGPP
GLES DPEPAALGSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16.

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTTCACCCAGACCTCACATTCCATTGGAAAGA
AGACTAAAAATGGTGTTCAAATGTGGACACTGAAGAGACAAATTCTTATCCTTTAACATAATCCTAATTCC
AAACTCCTGGGCTAGATGGTCTAAACTCTGCCCTGTGATGTCACTCTGGATGTCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTGACAGAAATCTCTGGAGGTATTCCACGAACACCACGAACCTCACCC
ACCATTAAACCACATACCGACATCTCCCAGCGTCTTCACAGACTGGACCATCTGTAGAGATCGATTTCAGA
TGCAACTGTGTACCTATTCACTGGGTCTAAACAAACATGTGATCAAGAGGCTGAGATTAACCCAGAACG
TTTAGTGGACTCACTTATTAAAATCCCTTACCTGGATGAAACCAAGACTAGAGATAACCGCAGGGCTCCG
CCTAGCTTACAGCTCTCAGGCTTGGCAACACATCTTTCATCAGAAAAGAGAACTAACAGAACTGCC
AACATAGAAATACTACCTGGGCAAACACTGTTATTATCGAAATCCTGTTATGTTCATATTCAATAGAGAAA
GATGCCCTCTAAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAAATGTACAGCGTCCCTACTGTT
TTGCCATCTACTTAAACAGAACTATATCTCTACAAACATGATTGCAAAATCCAAGAAGATGATTTAATAAC
CTCAACCAATTACAATTCTGACCTAAGTGGAAATTGCCCTCGTTATAATGCCCATTCCTGTGCC
TGTAAAATAATTCTCCCCTACAGATCCCTGTAATGCTTTGATGCGTGCAGAATTAAAGTTTACGCTTA
CACAGTAACTCTTCAGCATGTGCCCTAAGATGTTAAGAACATCAACAAACTCCAGGAACCTGGATCTGCC
CAAAACTCTGGCAAAGAAATTGGGATGCTAAATTCTGATTTCTCCCTGCCCTCATCCAATTGGATCTG
TCTTCATTTGAACCTCAGGTCTATCGTCATCTGAATCTATCACAAAGCATTTCTCACTGAAAAGCCTG
AAAATTCTGCGGATCAGAGGATATGTTAAAGAGTTGAAAAGCTTAAACCTCTGCCATTACATAATCTCAA
AATCTGAAGTTCTGATCTGGACTAACTTTATAAAATTGCTAACCTCAGCATGTTAAACAATTAAAGA
CTGAAAGTCATAGATCTTCAGTGAATAAAATATCACCTCAGGAGATTCAAGTGAAGTGGCTCTGCTCAAAT
GCCAGAACTCTGTAGAAAGTTATGAACCCCAGGCTCTGGAAACAATTACATTATTCAGATATGATAAGTATGCA
AGGAGTTGAGATTCAAAAACAAAGAGGCTTCTTCATGCTGTTAATGAAAGCTGCTACAAGTATGGCAGACC
TTGGATCTAAGTAAAATAGTATTTTGTCAGTCTCTGTTAATGCACTTTCTTCTCAAATGCC
AATCTGTCAGGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTCCAACCTTCTAGCAGAGCTGAGATATTG
GACTTCTCCAACAAACGGCTGATTTACTCCATTCAACAGCATTGAAAGAGCTCACAAACTGGAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTCATCAGAAGGAATTACTCATATGCTAAACTTACCAAGAACCTAAAGGTT
CTGCAGAAACTGATGATGAACGACAATGACATCTCTCCACCAGCAGGACCATGGAGAGTGTAGCTCTTAGA
ACTCTGAAATTAGAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAATCCCTAACGTTCTGCTCTGGAGTTTGTGATGGT
ATGCCCTCAAATCTAAAGAATCTCTTGGCAAAATGGCTCAAATCTTCAAGTGGAGAAACTCCAGTGT
CTAAAGAACCTGGAAACTTGGACCTCAGCCACAACCAACTGACCACTGCTCCCTGAGAGATTATCCAACGTCTCC
AGAACGCTCAAGAATCTGATCTTAAGAATAATCAAATCAGGAGTCTGACAAGTATTTCTACAAAGATGCC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAGACCAGCTCCAGAAAATGTCTC
AAACATCTGAAGATGTTGCTTGCATCATATCGTTCTGTGACCTGTGATGCTGTTGTGCTGG
GTTAACCATACGGAGGTGACTATTCTTACCTGGCACAGATGTGACTTGTGAGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTACCTTCC
TCTGTATCTCTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTCTGGATGTGTTGATATTACCAT
TTCTGTAAGGCAAGATAAAGGGTATCAGCGTCTAATATCAGAGACTGTTGCTATGCTTGTGTTGAT
GACACTAAAGACCCAGCTGACCGAGTGGGTTGGCTGAGCTGGCCTAACACTGGAAGACCCAGAGAGAAA
CATTTAATTATGTCAGGAAAGGGACTGGTACCGGGCAGCCAGTCTGGAAAACCTTCCAGAGCATA
CAGCTTAGCAAAAGACAGTGTGATGACAGACAAGTGAAGACTGAAAATTAAAGATAGCATTTC
TTGTCCTCATCAGAGGCTATGGATGAAAAGTTGATGTTGATTATCTGATATTCTTCAAGTGGAGCC
TCCAAGTTCTCCAGCTCCGAAAAGGCTGTGGAGTTCTGCTCTTGAGTGGCCTAACAAACCCGAAGCTCAC
CCATACTCTGGAGTGTCTAAAGAACCCCCCTGGCACAGACAATCATGTCAGGCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTCTTGCAAAACACAACACTGCCCTAGTTACCAAGGAGAGGCCTGGC

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FIGURE 358

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCTDVTLDVPKNHVIVDCTDKHLTEIPGGI
PTNTTNLTLTINHIPDISPASFHRLDHLEIDFRNCVCPIPLGSKNNMCIKRLQIKPRSFSGL
TYLKSLYLDGNQNLLEIPQGLPPSLLQQLSLEANNIFSIRKENLTELANIEIILYLGQNCYYRNPC
YVSYSIEKDAFLNLTKLKVLSLKDNNTAVPTVLPSTLTELLYLYNNMIAKIQEDDFNNLNQLO
ILDLSGNCPRCYNAPFCAPCKNNSPLOIPVNNAFDALTELKVRLHSNSLQHVPPRWFKNINK
LQEELDLSQNFIKEIGDAKFLHFLPSLIQLDLSFNFEQVYRASMNLSQAFSSLKSLKILRIR
GYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFQFKRLKVIDLSVNKISPSGDSSE
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKGQTLDLSKNS
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLLHSTAHEELHK
LEVLDISSIONSHYFQSEGITHMLNFTKNLKVQKLMMDNDISSLRTMESESRTLEFRGNH
LDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK
KLQCLKNLETLDLSHNQLTTVPERLSNCRSRLKNLILKNNQIRSITKYFLQDAFQLRYLDLSS
NKIQMIQKTSEPVNLNNLKMPLLHHNRFLCTCDAVWFVWWVNHTEVTI PYLATDVTCVGPAGA
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ
RLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLNLSQ
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLEKPFQSKFLQLRKRLC
GSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFKETV

Important features:

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

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FIGURE 359

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCCGTGCTCTGCTGCCGCTACTGCTAC
TGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGTGG
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCACAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCTCGCAAGGCCTACGCACGGCAGTGCCTGTGGGCCACAACA
AGGAGCGCGGGCGCCGCGCGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTCCGTGCTCCC
AATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGGCCGAAGATG
CTCAGGATTGCTTACCTGGTAACTGAGGCCCATCCTCCGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGGATTCCGGTTTCTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCGTGTGGAAACCCAGGCCCAACTCCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAACAACGTGAGGTCCCT
CCATTTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTACCTCCCCAAATCGA
CCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA
GCCAGAGAACTCTGGACCCCAAGATGTCCTGACAGGGCAAGGGAACTCCTACCCATG
CCCAGGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTGAGGTCTGGCCTCAGTT
TTCCAGGCCAGGACAAGCCAGGTGAGCTGAGGCCACACTGGACCACACGGGGCACACCTCCT
CCAAGTCCCTGCCCAATTCCCCAATACCTCTGCCACCGCTAACGCCACGGGTGGCGTGC
TGGCTCTGCAGTCGCTTGCCTGCCAGGTGCAGAGGCCCTGACAAGCCTAGCGTTGTCAGGGC
TGAACCTGGGCCCTGGTCATGTGTGGGCCCTCCTGGACTACTGCTCCTGCCCTCTGG
TGTTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTC
TCATCTCCCCACCCCTGCCCCAGCCCTAAACAAGATACTTCTGGTTAAGGCCCTCCGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCCTGGAGGCACAAGGCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACCGGGCCACACCTCTGCCCTCC
TCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCTCACTGCCTACCTGGCCTGGGCTGTCT
GCCACACAGCATGTGCCTCTCCCTGAGTGCCTGTAGCTGGGATGGGATTCCTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGTTCTTGAGTGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACCTGACTCTCAATAAAACCTGTCCAACCTGTGAA

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FIGURE 360

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLHYRAQVSPTASDMLHMRWDEEL
AAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKR PYQE GTPCSQCPSG
YHCKNSLCEPIGSPEADAQDL PYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSL
ATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSI LAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENS LDPKMSLTGARELLPHAQEEAEAEAEALPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATA NATGGRALALQSSLPGAEGPDKPSVVSGLNSGP
GHVWGPLLGLLLPPLVLAGIF

Important features:**Signal sequence:**

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 361

GACTAGTTCTTGGAGTCTGGGAGGAGGAAAGCGGAGGCCGGCAGGGAGCGAACCAAGGACTGG
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGAGAAGCGCAGGGCTGGAGCACCAACT
GGAGGGTCCGGAGTAGCGAGGCCGGGAAGGAGGCCATGGGGAGCCGGAGGGGGACTGCG
AGAGGACCCCGCGTCCGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGCTGCT
CCTGGGCCTGGCGGCCGGCTGCCCTGGACACAAGATCCCCAGCCTCTGCCCGGG
GCACCCCGGCCTCCAGGCACGCCGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG
CCGCGACGGCCCGGACGGCGGCCGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGG
ACTGCCGGGACCTCGAGGGGACCCGGGCCGAGGGAGAGGCCGGACCCGCCGGGCCACCGG
GCCCTGCCGGGAGTGCTCGGTGCCCTCCGCGATCCGCCCTCAGGCCAACGCGCTCCGAGAGCCG
GGTCCTCCGCCGTCTGACGCACCTTGCCCTCGACCGCGTGTGGTGAACGAGCAGGGACA
TTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTACTTCGCCGTCCA
TGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTGAAGAATGGCAATCCATTGCCCTC
TTTCTCCAGTTTCCGGGGGTGGCCAAGCCAGCCTCGCTCTCGGGGGGGCCATGGTGA
GCTGGAGCCTGAGGACCAAGTGTGGTGCAGGTGGGTGTGGTGAACATGGCATCTATGC
CAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTGCTTAGTGCCACTGCAAAGTGAGCTATGCTCTACTCCTAGAAGGAGGGTGTGA
GGCTGACAACAGGTATCCAGGAGGGCTGGCCCCCTGGAATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGAACAGTGGCTGTGCGATCA
GGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAAGACCAGAGGAGTGTGCTGTGCTGG
CAAGTGTAAAGTCCCCCAGTTGCTCTGGTCCAGGAGGCCACGGTGGGTGCTCTCTGGTC
CTCTGCTTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGCCGGCCCTTCAGAGAT
CACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAA

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FIGURE 362

MRPLLVLLLLGLAAGSPLLDDNKIPSLCPGHPGLPGTPGHHSQGLPGRDGRDGAPGAPG
EKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIÄSFFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA

Important features:

Signal sequence.

amino acids 1-15

N-myristylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 363

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGCT
TCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGCCA
GGGGAGGGTGACCAAGGCAGGCCCTGAGCGACGCTCCCCATGATGACGCCAACGGAAACTT
CCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCAAGGAATTGACCAACTCACCCC
AGAGGAAAGCCAGGCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGGGGACGGCGA
CGGCTGGGTGTCGCTGGCCGAGCTCGCGGTGGATCGCGCACACGCAGCAGCAGCACATACG
GGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGCGTGTGGTTGGGA
GGAGCTGCGCAACGCCACCTATGCCACTACGCGCCCGGTGAAGAATTGACGTGGAGGA
TGCAGAGACCTACAAAAGATGCTGGCTGGACGAGCGCGTTCCGGTGGCCGACCAGGA
TGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCCTCA
CATGCGGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAAGATGGCTATGT
CCAGGTGGAGGAGTACATCGCGGATCTGTAUTCAGCCGAGCCTGGGGAGGAGGAGCCGGCTG
GGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGGATGGGCACCTGGA
TGGGAGTGAGGTGGCCACTGGGTGCTGCCAGGACCAAGCCCTGGTGGAAAGCAA
CCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAAAGCGAAATCCTGG
TAATTGGAACATGTTGGCAGTCAGGCCACCAACTATGGCGAGGACCTGACCCGGCACCA
CGATGAGCTTGAGCACCGCGACCTGCCACAGCCTCAGAGGCCGCACAATGACCGGAGGAG
GGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAGGAGCAGATGCAGTCCAGGC
ATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTCTGTCCCTGTACACCCCCA
ACCCCAAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAACCTATTCTGACTGAGTCTCC
CAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTTAAGAACCGCCCCAACCCCTCCAG
CTCCAAATCTGAGCCTCCACCATAGACTGAAACTCCCTGGCCCCAGCCCTCTCCTGCCCTG
GCCCTGGCCTGGACACCTCCTCTGCCAGGAGGCAATAAGCCAGCGCCGGACCTTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 364

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT
AFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 365

GTCTGTTCCCAGGAGTCCTCGGGCGTGTGTCACTGGCCTGATCGCG**ATGGGGACAAAG**
GCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCTGTG
AAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAGTTGACCAAGGA
GACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGGTGACC
TTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACCATTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGATGGGATAGTG
ATGCCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCTGAATCCCACA
ACAGGAGAGCTGGTCTTGATCCCCGTGACCTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
CGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAATCTGGTTTTGGC
ATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCTG
GTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCTGATGTCTGTAGTTCACAGGATGCCATTGGTCTTACACCCACAGGGCC
CCTACTTCTCGGATGTGTTTTAATAATGTCAGCTATGCCCCATCCTCCTCATGCCCTC
CCTCCCTTCTACCACTGCTGAGTGGCCTGGAACCTGTTAAAGTGTATTCCCCATTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTCCCTCTAAGTAGACAGCAAAA
TGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTGAATAGG
TATCTTGAGCTGGTTCTGGCTCTTCCCTGTACTGACGACCAGGGCAGCTGTTCTAGA
GCAGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTGGTGTGACACTGGGGCCTTCCAT
CTCTGGGGCCACTCTCTGTCTTCCATGGGAAGTGCCACTGGGATCCCTGCCCCGT
CTCCTGAATACAAGCTGACTGACATTGACTGTGTGAAAATGGGAGCTTGTGTTGGA
GAGCAGTAGTAAATTTCAGAGAACCTGAAGCCAAAAGGATTAAAACCGCTGCTCTAAAGAAA
AGAAAAACTGGAGGCTGGCGCAGTGGCTCACGCCGTAACTCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTGGGAGTTGGGATCAGCCTGACCAACATGGAGAAACCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAAGAG
CAAAACTCCAGCTAAAAAAAAAAAAAA

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FIGURE 366

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPEENNPKLSCAYSGFSSPRVEWK
FDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGN SYGEVKVKL
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKD GIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGI
LVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEG EFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 367

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCTGGATCTAACACAAATGTGTATATGTGACACACAGGGAGCATTCAAGAATGAAA
TAAACAGAGTTAGACCCGGGGGTGGTGTGTTCTGACATAAATAAAATAATCTAAAGCAGCTGTCCTCC
CCACCCCCAAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCATTTCTC
TATAAAGGAGAAAGTGAAGCCAAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAAGT
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAATTAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACACAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAAGTTCTTCATCAACCTCCTTTTTAAAT
TTTATTCTCTTGGTATCAAGATCATGCGTTTCTTGTCTTAACCACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTTGAATTCCAGAACAGGACAAACACCAGATAAAATTATGAATGTTGAACAAGAT
GACCTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTCT
GCTGGCTCTCAACTTGTGGCTGGCTGGTCTGGTGCAGACCTGCCCCTGTGTGCTCTGCAGCAA
CCAGTTCAAGGATGATTGTGTTCGAAAAACCTGCGTGAAGGTTCCGGATGGCATTCCACCAACACACGGCT
GCTGAACCTCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGAACAATCGCTTACTACCATCCGAATGGAGCTTTGTATACTGTCTAAACTGAAGGAGCTGTT
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGTTAACAGAATTCTTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAACGGTCTGTTGAAGGCTGTCAACTTGAGGTATTGAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAATAGTAGGCTGGATCTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCAAAACTGTGATGATAACAGTCCCAGAT
TCAAGTGAACGGAATGCCCTTGACAACCTCAGTCAGTAGTGAGATCAACCTGGCACACACATAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGATCATCTAGAGCGGATACATTACATCACAACCCCTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTGAAACACAGCTTGTGTGCCGGT
TAACACTCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTACAAAGTGGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACGTGCAAGATAACAGGATGTACACATGTATGGTGAGTAA
TTCCGGTGGGAATACTACTGTTCAGCCACCTGAATGTTACTGCAGCAACACTACTCCTTCTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAAATGTGGGCTCCACTCC
AGTGGTCAGTGGGAGACCACCATGTAACCTCTCAGGATGAGGCACAGAGCACAAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCTGAAAGACTACAAAATCATCAT
TGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTCTACAAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTATTAATGTTGATGAGGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCATGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCC
CAACACACAAACAGTTAACACAATAAAATTCAATACACAGGTCAGTGCAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTGACACTGGCTAAATCTACTGTTCAAAAAACAAACAA
GACAGTTTATTAAGGAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAACAA
AAAAGAAAAGAAATTATTTATTAAAGTGTGATCTAAAGCAGACAAAAA

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FIGURE 368

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLVVAGLVRAQTCPSVCSNSQFSKVICVRKNLREVPDGIS
TNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDRRLTTIPNGAFVYLSKL
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDELD
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH
NPWCNCNDILWLSSWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVT EGMAELKC
RASTS LTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGNTTASATLNVTAATTTP
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKT
TKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTRTVEIIINVDEITGDPME SHLPMPAIEHEHLNHYNS
YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

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FIGURE 369

CAAAACTTGCCTCGGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCAGCCCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCTGTGGGGCGCTCGCGCCGGGCGCAGCAGGGAAAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCACACTGGTGTGAAACCGGGAGAGCCCCTGGTGGTCCCCTATCCCTCCTTATATA
GAAACCTCCACACTGGAAAGCAGCGCAGGGCAGGGCTCATGGTGTGAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACAAATGAAGGGAGGGAGGCCAGAACAGCCTGCC
TCCATCAGCCCTGGCGCCAGCGCATTGACTCGGCACCCCTGCAGGGACCATGGCCAGGCCGGTGTGC
TGCTCTGCTGCTGCCACAGCTGACCTGGACCTGTGCTGCCGTGAGGGCCCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGCCTGGCCAGCCCGAGCTGCCCCAGACTGTGCTGTTCCAGGAGGGCGTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCCCTGAGCACACCAACCACCTATCTCTGCAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGGAGCTCTCCGGCTGACCGGCTGGAGACACTGAACCTGCAAAACAACCGCTGA
CTTCCCAGGGCTCCCAGAGAACGGCTTGTGACATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCGCTTGTGCAAACGCCGTGACTGAGCTGTTGCTGCCAATATCTCACCAAGATCT
ATGGGCTCACTTTGGCCAGAACGCAAACCTGAGGTCTGTGACTGTGACAACAAACAGCTGGCAGACGCC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCTGTGAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGACCACTCAAGAACACAAGCTGGAGAAGATCCCCCGGGG
TCAGCGAGCTGAGCAGCCTGCCGAGCTACACCTGAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCAGCAACAAACCTGTCCTGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAAGAACGCCATCCGGAGCGTGGACCGAATGTGCTGACCCCC
GCAGCCTGGAGTACCTGCTGACAGCAACCGAGCTGCCGGAGCAGGGCATCCACCCACTGGCTTCCAGGG
TCAAGCGGTTGCAACACGGTGCACCTGTACAACAAACCGCTGGAGCCCTGCCCCAGTGGCTGCC
GCACCCCTCATGATCCTGCACAACCGATCACAGGATTGGCCGAGAACACTTGCACCCACTACTCCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGGCTGACCGCTGCCACCTGGCTGCCCTGAAATGTCC
GCTGCTGGACCTGTGGTGCACACGGCTGAGCAGTGGCTGCCACCTGGCTGCCCTGAAATGTCC
TCAAGCGCAATGAGCTGGCTGCCCTGGCACGAGGGCGCTGGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCCAGCCAGCCCTGGGCCCCCTGCCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGCAGAACAAACA
AGATTAGTGCCTGGCCCAATGCCCTGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGTGGACAGTGCTTCCGGAGGCTGAAGCACCTGCAAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAATTCCAAGGACCGTGGCGCTGGGGAGGAAAAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGGACAAGGTGATGCAGATGTGACCTAGGATGATGGACGCCGGACTTTCTGC
AGCACACGCCCTGTGTGCTGTGAGCCCCCCTACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGCCAGACACATGC
ACACACATCACACCCCTAAACACCCAGCTGCCACACACAACACTACCCCTCAAACCCACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAAGGGCTGCCCTGGCACACACAGGCC
TCCCCCTCCCTGCTGACATGTGCTGCTGATGCATACACACACACACATGCACAGTGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGGCCAGGCCAGAATCAGGCCATAGCAGCTGCCGTCTGCC
GTCCCATCTGCTGGCTCCGTTCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCC
GGAACCTCACAAAAGCTGGCTTTATTCTTCCCATCTTATGGGACAGGAGCCTTCAGGACTGCTGGCTGGCC
TGGCCCAACCTGCTCCTCCAGGTGCTGGGAGTCACCTGCTAAAGAGTCCCTCCCTGCCACGCC
CAGGCAGTTTCCAATGGCAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGGGCC
CAGGAGTGAAGCAGGGTGTGGGGCTGGGCTGAGCCAGGGAGGAAGGCCAGCTGCACCTAGGAGAACCTTT
GTTCTCAGGCCTGTGGGGAAAGTTCCGGTGCCTTAATTCTTATTCTTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTTCTGTTAGAAAAACTAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

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FIGURE 370

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRSG
GHSLSPPEENFAEEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLPEH
TNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHTLNLYLANNKTL
APRFLPNALISVDFAANYLTAKIYGLTFGQKPNLRSVYLHNNKLA DAGLPDNMFNGSSNVEVLI
LSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK
LSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSNQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYFLEELNLS
YNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEA ALARGALAGMA
QLRELYLTSNRLRSRALGPRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGI FLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE
EEEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 371

CACTTCTCCCTCTTCCTTACTTTCGAGAAACCGCGCTTCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG
CCGGGGAGACGGAGGTGCTGTGGTGGGGGGACCTGTGGCTGCTCACGCCCCCCACCTCCTCTGCAC
TGCCGCTCTCCGGAAGACCTTTCCCCTGCTCTGTTCTTCACCGAGTCGTGCATGCCCGGACCTGGCCGG
GAGGAGGCTTGGCCGGGGAGATGCTTAGGGGCCGGGGAGGAGCGGCCGGGGACGGAGGGCCGGAG
GAAGATGGGCTCCCGTGGACAGGGACTCTGCTGGCTACTGCCTGCTCTTGCCCTTGCCCTGGTCT
GAGTCGTGTGCCCCATGTCCAGGGGACAGCAGGAGTGGGAGGGACTGAGGAGCTGCCGTGCCCTCCGGACCA
TGCCGAGAGGGCTGAAGAACACATGAAAAATACAGGCCAGTCAGGACCAGGGCTCCCTGCTTCCGGTGCCT
GCGCTGCTGTGACCCCGTACCTCCATGACCCGGCACGCCGTGCCAGATCAACATCACTATCTTGAAGG
GGAGAAGGGTGACCGCGAGATGAGGCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGCCA
CACTGGACCAAAGGGCAGAAGGGCTCATGGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC
GGTGGCCGGAGAACAGCCATGCACAGCAACCAACTACTACCAGACGGTATCTCGACACGGAGTTGTGAACCT
CTACGACCACCTCAACATGTCACCGCAAGTTCTACTGCTACGTGCCGGCTCTACTTCTCAGCCTAACGT
GCACACCTGGAACAGAAGGGAGACCTACCTGCACATCATGAAGAACAGGAGGAGGAGGTGATCTGTTCGCGCA
GGTGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTTAG
CCTCTACAAGGGCGAACGTGAGAACGCCATCTTCAGCAGGAGCTGGACACCTACATCACCTTCAGTGGCTACCT
GGTCAAGCACGCCACCGAGCCCTAGCTGGCGGCCACCTCTTCTCGCCACCTCCACCCCTGCGCTGTGC
TGACCCCACCGCCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTGGCATTCACTGAGAACGCCCTGCACAC
ACAGAAAGCCAAGCGATGGTGTCCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACAG
GGCAGGGCACCCCGCAGAACCCCTCTGGACCTTCCGGCCCTCTGCACACATCCTCAAGTGAACCCCGCACGG
CGAGACCGGGTGGCGCAGGGCGTCCCAGGGTGGCAGCCGGCTCCAGTCCTTGAAATAATTAGGCAAATT
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAGAAAAGGGTTGTTATTGGCTTTCCAGGCCAG
CCTGCTGGCTCCCAAGAGAGAGGGCCTTTCAGTTGAGACTCTGCTTAAGAGAACATCAAAGTTAAAGCTCTGG
GTCAGGGAGGGGCCGGGAGAACACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACATTCTGAGGG
ATAGGTGGACCCCTGACATCCCCTGTCAGCTGGCCCTGCCCAGGGCTCTGCTGGTCTTCAGTCAGCTGCGAGGTGA
TGGGGCTGGGGCCAGCGTCAAGCTCCAGAGGGACAGCTGAGCCCCCTGCTGGCTCCAGGTGGTAGAA
GCAGCCGAAGGGCCTGACAGTGGCAGGGACCCCTGGCTCCCCCAGGCTGAGATGTTCTATGAGGGCAG
AGCTCCTGGTACATCCATGTTGCTGCTCCACCCCTGTCACCCAGAGCCCTGGGGTGGTCTCCATG
CCTGCCACCCCTGGCATGGCTTCTGTCGGCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCT
CTGTTTTATAAAACACCTCAAGCAGCACTGCACTCTCCATCTCCTCGTGGCTAAGCATCACCCTCCACG
TGTGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTCATCCAGGCCCTGTGACCA
GTAGCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAGCTGAAAGGGCTAGAAAGCTCCGTTGTCT
GTTTCAGGCTCTGTGAGGCTCAGTCCTGAGACAGAGTCAGAGGAAGTACACGCTCAACCCGTGTCA
GGATTCACTCTCAGGAGCTGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAAGGACCAGCTGGAGCAGGG
TTGCGGTGTCTCACGGTGTCTGCCCTGCCATGGCCACCCAGACTCTGATCTCAGGAACCCCATAGCCCC
TCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCCCAAAACCCCGCTGCCCTTC
TCCCTCCCCCATCCCCACCTGGTTTGACTAACTCTGCTTCCCTCTGCGGGCTGGCTGCCGGATCTGGGG
TCCCTAAGTCCCTCTTTAAAGAAACTCTGCGGGTCAAGACTCTGAAGCCAGTTGCTGTGGCGTGCCCGGAAG
CAGAGGCCACACTCGCTGCTTAAGCTCCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

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FIGURE 372

MGSRGQGLLLAYCLLAFAASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRPS
QDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG
PKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFHGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK
GERENAIFSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

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FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCGCGGCTGCCTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGGAA
GCATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC
ACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATCCTGTAAAACCCAAAG
ATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAGAGTTCT
TCAGTTCTGAAAATGTTAAAGTGTGTTGAGTCATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACTGGTTCTTCC
TTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAAAAAAGGATC
CATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCTCAATATCCCAG
AAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA
ATACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG
AAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAATGATGCATTGGTTCT
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTGTA
TAGGACGTGTGTTGTCATTATTTGTTAGTAGTAACATACATCCAATACAGCTGTATGTTCTT
TTCTTCTAATTGGTGGCAGTGGTATAACCACACATTAAAGTCAGTAGTACATTTTAAA
TGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATGTGTTGGAAAGAAGTGTGTTTA
AGAATAATAATTGCAAATAAACTATTAAATAATTATATGTGATAAAATTCTAAATTATGA
ACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTAAAAAATTTAACAGGTCTTA
GCCTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTGTGATTAAAGTAAAACCTTGT
CTGTGTGTTCCCTTACTTCTAATACTGATTATGTTCTAAGCCTCCCCAAGTCCAATGGAT
TTGCCTTCTCAAAATGTACAACAAAGCAACTAAAGAAAATTAAAGTGAAGTTGAAAAT

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FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
KPKDVLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI
IENLKYLFLKKDPSQPFLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSILLNIPEKCPHQGGMIWKISEDKQLAV
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTBNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 375

GTTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTGCACAAGCTGAGAGAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAACCGAACCTGACAAAAAAGAAGAAAAGAAGAAGAAA
AAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTGGCAATCTCACGGG
GCTGGCTGCTGTCTCTCCAAGGAGTGCCCGTGCAGCGGAGATGCCACCTCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCCTCAGGTGCACTATTGACAA
CCGGGTCAACCGGGTGGCCTGGCTAAACCGCAGCACCATCCTATGCTGGGAATGACAAGTG
GTGCCTGGATCCTCGCGTGGTCTTGAGCAACACCCAAACGCACTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA
GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATTCTTCAGATAT
CTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTGAGTGAAGACGAATACTTGG
AATTCAAGGGCATCACCCGGAGCAGTCAGGGACTACGAGTGCAGTGCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACATCCACCATACATTCAGAAGCCAA
GGGTACAGGTGTCCCCGTGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGTGAAGT
GGAAAACAGACCTTCCTCTCAAAACTCATCTTCTCAATGTCTGAACATGACTATGGAA
CTACACTTGCCTGGCCTCCAACAAGCTGGCCACACCAATGCCAGCATCATGCTATTGGTCC
AGGCCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCCTGGCTGCC
TCTTCTGGTCTTGCACCTGCTTCTCAAATTTGATGTGAGTGCCACTTCCCCACCCGGAAAG
GCTGCCGCCACCACCAACACAAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGACAGAAATTGAGGGAGGGAAACAAA
GAATACTTGGGGGGAAAAGAGTTTAAAAAAGAAATTGAAAATTGCCTTGAGATATTAGG
TACAATGGAGTTTCTTCCAAACGGGAAGAACACAGCACACCCGGCTGGACCCACTGCA
AGCTGCATCGTCAACCTCTTGGTGCAGTGTGGCAAGGGCTCAGCCTCTGCCACAGA
GTGCCCGTCAGCGAGGTGAGCTGCCATCCAAATTCAATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGGCCAAGCGTGGCCTGGGGCACTTGGTAGACTGTGCCACCAAG
GCGTGTGTTGTGAAACGTGAAATAAAAGAGCAAAAAAAA

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FIGURE 376

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRV
TRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISP KAVGFVSEDEYLEIQ
GITREQSGDYECASNDVAAPVVRVKVTVNYPYISEAKGTGVPVGQKGTLQCEASAVPSAE
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNLGHTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Important features:

Signal peptide:

amino acids 1-28

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FIGURE 377

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGAA
ATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACACCTACCGTCCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCACACA
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACCAACAC
AAGTTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTCCCTGATGAA
GGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCAGAAGATA
CAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTCAGATTCTCCCTCTGGGCT
GTGGAGTATGTGGGAAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTCTCCCCAAAAC
AATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAAATTACAGCTGCCCTGGTGAGG
AACCTGTCAGTGAATGGAAAGTGTATCATTATGCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGCTAAAAGTAGGGGAAGTGTACTGTTGACCTTGGAGAG
GCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATCATTAAGCATGGCCTCGCTTAGAAGTGCATCTGAGAAAGTA
GCCAGAGACAATGGACTATGTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA
ACTCATTCACAGTTATCATCACCTCCGTAGGACTGGAGAAGCTGCACAGAAAGGAAAATCA
TTGTCACCTTAGCAAGTATACTGGAATATCACTATTTGATTATATCCATGTTCTCTC
TTCTATGGAAAAAATCAACCTACAAAGTTATAAAACAGAAACTAGAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTAAACATTTCAGGCCATGAAGATGCTCTGGATGACTCGGAATA
TATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTTGCTATGGGCAAGATTGACAGTACAGTGTATGAAGTTATTGAGCACATC
CCTGCCAGCAGCAAGACCATCCAGAG**TGA**ACTTCTAGGCTAAACAGTACATTGAGTGAA
ATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGTATTTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTTACTCATTATCCTTACATGCAGAATAGAGGCATTATGCAA
TTGAAGTGCAGGTTTTCAGCATATACACAATGTCTGTGCAACAGAAAAACATGTTGGGAA
ATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGTTCT
CATAAGTTGTATGAATACTCTACAAACCTCAATTAGTTACTCTACACTTCACTATC
ATCAACACTGAGACTATCCTGTCACCTACAAATGTGGAAACTTACATTGTTGATTTTC
AGCAGACTTGTATTAAATTAAATTAGTGTAAAGAATGCTAAATTATGTTCAATT
ATTCCAAATTCTATCTTGTATTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA
AAACTATGCCTCTCTTTTCAATCACCAGTAGTATTGAGAAGACTTGTGAACACTT
AAGGAAATGACTATTAAAGTCTTATTGTTCAAGGAAAGATGGATTCAAATAAAATT
ATTCTGTTTGCTTTAAAAAAAAAAAAAA

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FIGURE 378

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS
VVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQKIQVTVDPPVTKPVVQIHPPSGAVEY
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEIGNYSCLVRNPVSEMESDIIMPII
YYGPYGLQVNSDKGLKVGEGVFTVDSLGEAILFDCSADSHPPNTYSWIRRTDNNTYIIKHGPRLEVASEKVAQKTM
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG
RPETEYRKAQTFSGHEDALDDFGIYEFPDVSGVSRIPSRSVPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

Important features:

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 379

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTCAGTCATACTTCACATGGCACAA
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTATATTATGTTAAATCAGTTTTGTT
CTCACGGCTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAACAGC
GCACATGCGTTCAAAATAAGAGCAAATTGCTCTAAACACAGGAAAGACCTGAAGCTTAA
TTAAGGGTTACATCCAACCCCAGAGCGCTTGTGGCACTGATTGCTCCAGCTTCTGCGTC
ACTGCGCGAGGGAGAGGGAGAGGGATCCAGGC~~T~~AGACATGTATAGACACAAAAACAGCTG
GAGATTGGGCTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAAGTCCCCAAACATTGAT
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAACGCTCCAGTCAGCCCACAA
GATGCCATTGTC~~CCCC~~GGCCTCTGCTGCTGCTCTCCGGGCCACGGCCACCGCTGCCCT
GCCCTGGAGGGTGGCCCCACC~~GG~~CGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG
GAAAAGCAGCCTCCTGACTTCC~~T~~CGCTTGGTGGTTGAGTGGACCTCCAGGCCAGTGCCGG
GCCCTCATAGGAGAGGAAGCTCGGAGGTGGCCAGGC~~GG~~CAGGAAGGC~~G~~CACCCCCCAGCA
ATCCCGCGCCGGACAGAATGCCCTGCAGGAAC~~T~~CTTCTGGAAGACCTTCTCCTGCAA
ATAG

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FIGURE 380

MYRHKN SWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLS
GATATAALPLEGGPTGRDSEHMQEAGIRKSSLTFLAWWF EWTSQASAGPLIGEEAREVARR
QEGAPPQQSARRDRMPCRNFFWKTFS SCK

Important features:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 381

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCGGCTGCGGCCCGGCC
GCGCCGCCAACCCCCAACCCCCGGCCCGGCCCGCCCTAGCCCCCGCCCGGGCCCGGCC
CCGCGCCCAGGTGAGCGCTCCGCCGCCGAGGCCCGCCCCGGCCCGCCCCGCCGCC
CGGCCGGCGGGGAACCGGGCGGATTCCCTCGCGTCAAACCACTGATCCCATAAAACATTC
ATCCTCCCGGCCCGCGCTGCGAGCGCCCGCCAGTCCGCGCCGCCGCCCCGCCCCGCC
TGCGCCCTGCGGCCCTGCGCACCCGCGGCCGAGCCCAGCCAGAGCCGGCGGAGCAGCG
CGCCGAGCCTCGTCCCGCGGCCGGGCCGGCGTAGCGGCCGCGCTGGATCGGAC
CCGGCCGCGGGAGACGGCGCCGCCGAAACGACTTCAGTCCCCGACGCGCCCCGCCA
ACCCCTACG**ATGA**AGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGAGCCAAGGTG
ACGACAAGCTCCCCCAGCAGGGCTGCAGGCTGTGCCGTGGCATCCCTGCTGCCAGCCAG
CGCATCTTCTGCACGCAACCGCATCTCGATGTGCCAGCTGCCAGCTCCGTGCCGC
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCATTGATGCGGCTGCCCTCACT
GCCCTGGCCCTCCCTGGAGCAGCTGGACCTCAGCGATAATGCAAGCTCCGGTCTGTGGACCC
GCCACATTCCACGGCCTGGGCCCTACACACGCTGCACCTGGACCGCTGCCCTGCAGGAG
CTGGGCCGGGCTGTTCCCGGCCCTGGCTGCCCTGCACTACCTCACCTGCAGGACAACCG
CTGCAGGCACTGCCTGATGACACCTCCCGCACCTGGCAACCTCACACACCTCTGCAC
GGCAACCGCATCTCCAGCGTGCCTGGAGCGCGCTTCCGTGGCTGCACAGCCTGACCGTCTC
CTACTGCACCAGAACCGCTGGCCCATGTGCACCCGATGCCCTCCGTGACCTGGCCGCCTC
ATGACACTCTATCTGTTGCCAACATCTATCAGCGCTGCCACTGAGGCCCTGGCCCCCTG
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGACTGCCGGCACGCCA
CTCTGGGCCTGGCTGAGAAGTCCCGGCCCTCCCTCCGAGGTGCCCTGCAGCCTCCGCAA
CGCCTGGCTGCCGTGACCTCAAACGCCCTAGCTGCCAATGACCTGCAGGGCTGCCGTGTGGCC
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCACCGATGAGGAGCCGCTGGGCTTCCC
AAGTGCTGCCAGCCAGATGCCGTGACAAGGCCCTAGTACTGGAGGCCCTGGAAGACCAGCTCG
GCAGGAATGCGCTGAAGGGACGCGTGCCTGGACAGGCCGCCGGCAACGGCTCTGGC
CCACGGCACATCAATGACTCACCTTGGACTCTGCCTGGCTTGCTGAGCCCCGCTCACT
GCAGTGCGGCCCGAGGGCTCCGAGCCACCGAGGTTCCCCACCTCGGGCCCTGCCGGAGGCCA
GGCTGTTACGCAAGAACCGCACCCGAGGCCACTGCCGTCTGGCCAGGCAGGCAGGGGGT
GGCAGGACTGGTGAECTAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC
CTGGCCCTGGCGCTGGTGTGGACAGTGTGCTGGGCCCTGCT**GA**CCCCCAGCGGACACAAGA
GCGTGCCTAGCAGCCAGGTGTGTACATACGGGGTCTCTCCACGCCGCCAGCCAGCCGG
GCCGCCGACCGTGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCCCTGCCGCCGCCACC
CCCATCTCCACCCCCATCATGTTACAGGGTTCGGCCAGCGTTGTTCCAGAACGCCGCTC
CCACCCAGATCGCGGTATATAGAGATATGATTTTACTGTGTAAAAATATCGGACGA
CGTGAATAAAGAGCTTTCTTAA

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FIGURE 382

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPGIPAASQRIF
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATF
HGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR
ISSVPERAFRGLHSMDRLLLHQNRVAHVPHAFRDLGRLMTLYLFANNLSALPTEALAPRLAL
QYLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVATGP
YHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH
INDSPFGTLPGSAEPLTAVRPEGSEPPGFPTSGPDRRGCSRKNRSHCRLGQAGSGGGGT
GDSEGSGALPSLTCSLTPGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 383

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTAAGAAGGGGGAGTCCTGAACCTGTCTG
AAGCCCTTGTCCGTAAGCCTGAACTACGTTCTAAATCTATGAAGTCGAGGGACCTTCGCTGCTTTGTAGGG
ACTTCCTTCTGCTTCAGAACATGAGGCTTTCTTGTGGAACCGGGCTTGACTCTGTCGTCACTTCTTGA
TTGGGGCTTGATCCCTGAACCAGAAGTGAAGGAAATTGAAGTCTCCAGAAGCCATTCACTGCCATCGCAAGACCA
AAGGAGGGGATTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCCATTGGTTACCCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA
AAGGAATGTGTAGGAGAGAAGAGAAAGCTCATCATTCCCTGCTCTGGGCTATGAAAAGAAGGAAAGGTA
AAATTCCCCCAGAAAGTACACTGATATTAATATTGATCTCCTGGAGATTGAAATGGACCAAGATCCATGAAT
CATTCCAAGAAATGGATCTTAATGATGACTGGAAACTCTCTAAAGATGAGGTTAACGATATTTAAAGAAGGAGT
TTGAAAAACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTGGTGGAGGATATTTGATAAAGAAGATG
AAGACAAAGATGGTTTATATCTGCCAGAGAATTACATATAAACACGATGAGTTAGAGATAACATCTACCC
TTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTAAAGAACATTTATTTTATACAATGTTCTTCT
TGCTTGTCCCCCTATTTTATATTTCTGACTCCTATTAAAGAACCCCTTAGGTTCTAAGTACCCATT
CTTCTGATAAGTTATGGGAAGAAAAGCTAATTGGTCTTGAATAGAAGACTCTGGACAATTTCACTTC
ACAGATATGAAGCTTGTACTTCACTTATAAAATTTAAAGTGTGAACTGGGAATATACCACGACATGA
GACCAGGTTATAGCACAAATTAGCACCCATATTCTGCTTCCCTCTATTCTCCAAGTTAGAGGTCAACATT
GAAAAGCCTTTGCAATAGCCAAGGCTGCTATTTCATGTATAATGAAATAGTTATGTGTAACTGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAATGGTTGGACCTGACTTGTAAATGGCTACTGCTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAACAAGGTTAATGCCAGGCATGGTGGCTATGCCGTAAATCCCAGCACTTGGGA
GGCTGAGGCAGGGCGGATCACCTGAGGTTGGAGTTGAGACCAGCCTGACCAACACGGAGAAACCCATCTC
TAAAAATACAAAGTAGCCCGCGTGGTGTGCGTGCCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCAGGAA
TCACTTGAACCCGAGGCCAGGTTGCGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAA
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG
CTCCTAGTGATTGGTGGCCTATTATGATAAAATAGGACAAATCATTATGTGAGTTCTTGTAAATAAAATGTA
TCAATATGTTAGATGAGGTAGAAAGTTATTTATATTCAATATTACTTCTTAAGGCTAGCGGAATATCCTT
CCTGGTTCTTAATGGGTAGTCTATAGTATATTACTACAATAACATTGTATCATAAGATAAAAGTAGTAAACCA
GTCTACATTTCCCATTCTGCTCATCAAAACTGAAGTTAGCTGGGTGGCTCATGCCGTAAATCCAG
CACTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGCCAACATGGTAAACCT
TGTCTCTACTAAAAATACAAAATTAGCCAGGCAGGGTGGCAGACACCTGTAGTCCAGCTACTCAGGGAGGCTGA
GACAGGAGATTGCTGAACCCGGGAGGCAGGTTGCAAGTGAAGCCAAAGATTGTGCCACTGCACTCCAGCCTGG
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAAACCTA
TCCTGGATT

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FIGURE 384

MRLFLWNAVLTLFVTSILGALIPEPEVKIEVLQKPFICHRKTGGDLMLVHYEGYLEKDGSLF
HSTHKHNNGQPIWFTLGLILEALKGWDQGLKGMCVGEGRKLIIPPALGYGKEGKGKIPPESTLI
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHDALVEDIFD
KEDEDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

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FIGURE 385

CTCCCACGGTGTCCAGCGCCAGAATGCGGCTTCTGGCCTGCTATGGGTTGCCTGCTGCTC
CCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAATCAGCGGTTGAAGGGACACTGTGTCC
CTGAGTCACCTACAGGGAAAGAGCTGAGGGACCACCGAAGTACTGGTGCAGGAAGGGTGGG
ATCCTCTCTCGCTCTGGCACCATCTATGCAGAAGAAGAGCCAGGAGACAATGAAG
GGCAGGGTGTCCATCCGTGACAGCCAGGAGCTCGCTATTGTGACCCGTGGAACCTC
ACCTGCAAGACGCTGGGAGTACTGGTGTGGGTCGAAAAACGGGCCGATGAGTCTTA
CTGATCTCTGTTGCTTTCCAGGACCTGCTGCTCCCTCCCTCTCCACCTCAG
CCTCTGGCTACAACACGCCTGCAGCCAAGGCAAAGCTCAGCAAACCCAGCCCCAGGATTG
ACTTCTCTGGCTCTACCCGGCAGCCACAGCCAAGCAGGGGAAGACAGGGCTGAGGCC
CCTCATTGCCAGGGACTTCCCAGTACGGGACAGAAAGGACTCTCAGTACACAGGAACCTCT
CCTCACCCAGCGACCTCTCCTGCAGGGAGCTCCGCCCATGCAGCTGGACTCCACC
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAACAGCCAGGGTGTCCATCCG
ATGGTCCGCATACTGGCCCAGTCCTGGTGTGCTGAGCCTCTGTGAGCCGAGGCTGATC
GCCTCTGCAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGGG
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAGGAAGCCCTCCAGGCCCT
GAGGGGAGGTGATCTCGATGCCTCCACACATCTGAGGAGGAGCTGGCTTCTCGAAG
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCAGGCCAGTGAAGCAGTATGGCTGGC
TGGATCAGCACCAGATTCCGAAAGCTTCCACCTCAGCCTCAGAGTCCAGCTGCCGGACTCC
AGGGCTCTCCCCACCCCTCCCCAGGCTCTCCTCTGATGTTCCAGCCTGACCTAGAGCTT
GTCAGCCCTGGAGGCCAGAGCGGTGGCCTGCTCTCCGGCTGGAGACTGGGACATCCCTGAT
AGGTCACATCCCTGGCAGAGTACCAAGGCTGCTGACCCCTCAGCAGGGCCAGACAAGGCTCAG
TGGATCTGGCTGAGTTCAATCTGCCAGGAACCTCTGGCCTCATGCCAGTGTGGACCC
GCCTCCTCCACTCCAGACCCACCTTGCTCTCCCTCCCTGGCGTCTCAGACTTAGTCCA
CGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCTGGGTGAGACTGGGATTCTGGCTT
CTCTTGAAACCACCTGCATCCAGCCCTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCA
CCAAGACCCACCAAAACCATCTCTGGCTGGTGCAGGACTCTGAATTCTAACAAATGCCAGT
GAAGTGCACCTTGAGTTGAGGGCAGTGGCCTGATGAACGCTCACACCCCTCAGCTTAG
AGTCAGCATTGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTCTGTGACACCCA
GATCCACGTGGGACTCCCTGAGGCCTGCTAAGTCCAGGCCTGGTCAGGTGCACAT
TGCAGGATAAGCCCAGGACCAGCACAGAAGTGGTGCCTTNCCATTGCCCTCCGGNCCA
TGCCTCTGCCTTGAAAAAATGATGAAGAAAACCTTGCTCCTTGTCTGGAAAGGG
TTACTTGCTATGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACAGAGTGCACGTAGGTGT
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACTGAAGGTGACTCCGAGTCCAGCCCCCTG
GAGAAGGGTGGGGTGGTGGTAAAGTAGCACAACACTATTTTTCTTTCCATTATT
ATTTTTTAAAGACAGAATCTCGTGTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCA
AACTCCGCCTCTGGTTCAAGTGTGATTCTCTGCCCTCAGCCTCCGAGTAGCTGGGATTACAG
GCACGCACCACACACCTGGCTAATTTGTACTTTAGTAGAGATGGGTTTACCATGTTG
GCCAGGCTGGCTTGAACTCCTGACCTCAAATGAGCCTCCTGCTCAGTCTCCAAATTGCCG
GGATTACAGGCATGAGCCACTGTGTCTGCCCTATTCCTTAAAAGTGAATTAAGAGTTG
TTCAGTATGCAAAACTGGAAAGATGGAGGAGAAAAGAAAAGGAAGAAAAAATGTCACCCA
TAGTCTCACCAGAGACTATCATTATTCGTTTGTGTACTCCCTCACTTTCTTCTTC
ACATAATTGCCGGTGTCTTTTACAGAGCAATTATCTGTATATAACAACTTGTATCCTGC
CTTTCCACCTATCGTCCATCACTTATTCCAGCACTTCTGTGTTTACAGACCTTTT
ATAAATAAAATGTTCATCAGCTGCATAAAAAAAAAAAAAAA

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FIGURE 386

MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGILFSRCSG
TIYAAEEGQETMKGRVSIRDSRQELSIVTLWNLTLDAGEYWCGVEKRGPDESLLISLFVFP
GPCCPPSPSPTFQPLATTRLQPKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ
YGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTAEDTSPALSSGSSKPRVSIPMVRILAPV
LVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLRLTAEEKEAPSQAPEGDVISMP
PLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

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FIGURE 387

GC GCCGGGAGCCCATCTGCCCCAGGGCACGGGGCGCGGGGCCGGCTCCGCCGGCACATG
GCTGCAGCCACCTCGCGCGACCCCCGAGGCAGCGCCAGCTCGCCCGAGGTCCGTGGAGG
CGCCCGGCCGCCCGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGTCCGGGATCGGG
ATGTCCCTCCTCCTCTCCTCTTGCTAGTTCTACTATGTTGGAACCTTGGGACTCACACT
GAGATCAAGAGAGTGGCAGAGAAAAGGTCACTTGCCCTGCCACCATCAACTGGGCTTCCA
GAAAAAGACACTCTGGATATTGAATGGCTGCTACCGATAATGAAGGGAACCAAAAAGTGGT
ATCACTTACTCCAGTCGTATGCTACAATAACTGACTGAGGAACAGAAGGGCCAGTGGCC
TTTGCCTCCAATTTCCTGGCAGGAGATGCCTCCTGCAGATTGAACCTCTGAAGCCCAGTGAT
GAGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCCTACGTGTGGAGGCCATGTCATCTA
AAAGCTTAGTGAGACCATCCAAGCCAAGTGTGAGTTGAAGGAGAGCTGACAGAAGGAAGT
GACCTGACTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA
ATCCGAGAGAAAGAGGGAGAGGATGAACGCTGCCTCCCAAATCTAGGATTGACTACAACCAC
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACAGTCAGCA
GGCAACGAAGCTGGAAAGGAAAGCTGTGGTGCAGTAACGTACAGTATGTACAAAGCATC
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTCTCTGGTG
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT
CGAGAAGATGCTGAAGCTCCAAAGCCCCTTGAAACCCAGCTCCTCTCAGGCTCT
CGGAGCTCACGCTCTGGTTCTTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG
CGGACACTGTCACACTGACGCAGCACCCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG
GGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCCTCCAAACGGCT**TGA**ATTACAATGGAC
TTGACTCCCACGCTTCTAGGAGTCAGGGCTTGGACTCTCTCGTCATTGGAGCTCAAGT
CACCAGCCACACAACCAGATGAGAGGTCTAAGTAGCAGTGAGCATTGCACGGAACAGATT
CAGATGAGCATTTCCTATACAATACCAAAGAAAAGGATGTAAGCTGATCTGTA
AAAAGGCATTTATTGTGCCTTAGACCAGAGTAAGGGAAAGCAGGAGTCAAATCTATTGT
TGACCAAGGACCTGTGGTGAGAAGGTTGGGAAAGGTGAGGTGAATATACTAAACTTTAAT
GTGGATATTGTATCAGTGCTTGATTACAATTTCAGAGGAAATGGGATGCTGTTGT
AAATTCTATGCATTCTGCAAACATTGGATTATTAGTTATTCAAGACAGTCAAGCAGAAC
CCACAGCCTATTACACCTGTCTACACCAGTACTGAGCTAACCAACTCTAAGAAACTCCAAA
AAAGGAAACATGTGTCTTCTATTCTGACTTAACCTTGTCTAAGGTTGGATTTAATT
TCAAGGGAGTTGAAATAGTGGAGATGGAGAAGAGTGAATGAGTTCTCCACTCTATACTA
ATCTCACTATTGTATTGAGCCAAAATAACTATGAAAGGAGACAAAATTGTGACAAAGGA
TTGTGAAGAGCTTCCATCTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA
ATGGAGCAATTGTGGATTCCCTCAAATCAGATGCCCTAAGGACTTCTGCTAGATATT
CTGGAGGAGAAAATACAACATGTCATTATCAACGTCTTAGAAAGAATTCTCTAGAGAAA
AAGGGATCTAGGAATGCTGAAAGATTACCAACATACCATTATAGTCTTCTGAGAAA
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTCTCTTA
ATATGTCAAGGAAGGTAGCCGGGATGGTGCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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FIGURE 388

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLTDNEGQNQKVV
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL
KVLVRPSKPCELEGELETGSDLTQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH
PGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV
WLLIRRKDKERYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANSASRSQ
RTLSTDAAAPQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPQSRAFQTV

Important features:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 389

GC GG CAC CTG GA AG **ATG** CG CCC ATT GG CT GG TGG CCT GCT CA AG GT GG TTT CG GGT CTT CG
CCT CCTT GT GT GC CT GG TATT CG GGG TAC CT GCT CG CAG AG GCT CATT CCAG AT GC ACCC CT GT
CC AG TG CT GC CT AT AG CAT CC CG CAG CAT CG GG AG AG GC CT GT CCT CA AA AG CT CC AG TCCC CA
AA AG GC AAAA AT GT GACC ACT GG ACT CC CT GC CC AT CT GAC AC CT AT GC CT AC AG GT TACT CA
GC GG AG GT GG CAG AAG CA AGT AC GC CAAA AT CT GCTT GAG GATA AC CT ACT TAT GG GAG AAC
AG CT GG AA AT GT TGC CAG AG GA AT AA AC AT TG CC ATT GT CA ACT AT GT AACT TGG GAG AT GT GA
CA GCA AC AC GAT GT TT GAT AT GT AT GA AG GC GATA ACT CT GG ACC GAT GAC GAG CACA AG TT AT TC
AG AG TG CT GC TCC AAA AT CC CT GCT CTT CAT GG TGA CCT AT GAC GAG CACA AG ACT GA
AT AAC GAT GC CA AGA AT GC CAT AGA AGC ACT TG GA AG TA AGA AA AT CAG GA AC AT GAA AT TC
GG TCT AG CT GG GT ATT TATT GCA GCA AA AGG CT TG GA ACT CC CT CC GAA AT TC AG AG GAG AAA
AG AT CA ACC ACT CT GAT GCT AAG AACA CAG AT ATT CT GG CT GG CTC GCA GAG AT CC CAG AT AG
AAG GCT GC AT ACC CAA AGA AC GA AGC **TG A** ACT GC AG GG CT CT GAG TA AT GT TT CT GT ATA
AA CA AA AT GC CAG CT GG AAT CG CT CA AGA AT CT TATT TT CT AA AT CC A AC AG CC CAT ATT GAT
GAG TATT TT GG TT GT TGT AA ACCA AT GA AC AT TG CT AG TT GT AT CAA AT CT GG TAC GCA
GT ATT TT AT ACC AGT ATT TAT GT TAG TGA AG AT GT CA ATT AG CAG GAA ACT AAA AT GA AT GG
AA ATT CT TAAAAA AAAAAA

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FIGURE 390

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC
FDMYEGDNGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRSSWV
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAAEIQIEGCIPKERS

Important features:

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 391

GGGGGCTTCTGGCTGGACACCTGCCCAAGGACCGGCCCTGGAGGGTCGCCGGAAAGGG
AGGAAGAAGGAAGGGCGGGCCGGCCCCCTGCGCCGCCCTGCGCCTCTGCCCTGCTCCGCC
AGCCCAGCCAGCCCCGCGGGCGGTACACCGCAGCCAGCCGCCCTCCGCGCCAAGCGCCTG
CTGTGCCCTGCCCTGCCCGCCAGCTCTGCCCGCAGCCGCCGGCGCCCCGGTACCGTGACCT
GCCCTGGCGCGGGCGGAGCAGGATGCTCCGCCGGGACCCTAACCCAGCGCTGCCCTGGTCTCTGCC
AGT GACCTCTGCCGGGTCGGAGCCCAGGGCGCAGCCCTGAGGACCTGATTATTACGGGAGCAGGAGATCTGGAG
CCGGGAGCCCTACTACCGCGGCCCGAGCCGAGCTCGAGACCTCTCCGCCCTGCCCTGCCGGGGGCC
GGAGTGGGAGCGCGCCCGCAGGAGCCCAGGCCGCCAAGAGGGCACCAAGGCCAAGAAAGCTCCAAGAGGA
GAAGTCGGCTCCGGAGCGCCCTCACAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGA
GGCTGCCAACGATGATCACAGTGTCCGTGAGGATGTCAGAGAGATGGCCACCTCTGGTCTGGA
AACCTAAAAATCACAGACTTCAGCTCCATGCCCTCACGGCTGAAGCGCTATGCCCTGGGGGACATCGAGGGAG
ACTCAACATCCAGGGGGCATTAATGAAAATGATTTATGACGGAGCGTGTGCGGGAGAATGACCTCA
GCAGTGGATTGAGTGGATGCTCGGCCCTGACCAGATTCACTGGTGTATCACTCAAGGGAGGAACCTCCCTG
GCTGAGTGAATGGTGCACATCCATAAGGTATGGTGTGAGCAATGACAGCCACAGTGGTCACTGTTAAGAATGG
ATCTGGAGACATGATATTGAGGGAAACAGTGAAGAGGAGATCCCTGTTCAATGAGCTACCGTCCCCATGG
GCCCGCTACATCCGATAAACCTCAGTCTGGTTGATAATGGGAGCATGCAATGAGAACATGGAGATCTGG
CTGCCACTGCCAGATCTAATATTATCACCGCCGGAACGAGATGACCAACTGATGACCTGGATTAA
GCACCAATTATAAGGAAATGCCAGTGTGATGAAAGTTGATGAAATGTGCTCAATATCACAGAATTAA
CAACATTGAAAAAGCCACCAGGGCTGAAGCTGTATGCTGGAGATCTCAGATCACCTGGGGAGCATGAAGT
CGGTGAGCCGAGTCCACTACATCGGGGGCCACGGAATGAGGTGCTGGCCGGAGCTGCTGCTGCTG
GGTGCAGTCTGTGTCAGGAGTACTTGGCCGGAATGCGCAGTGTCCACCTGGTGGAGGAGACGGGATTCA
CGTCCTCCCTCCCTCAACCCCGATGGTACAGAGAAGGCCCTACGAAGGGGCTGGAGCTGGGAGGTGGTCCCT
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACTTCTGATTTAACACCGCTGCTCTGGGAGGCAGA
GGATCGACAGAATGTCCCCAGGAAAGTCCAACTACTATATTGCAATCCCTGAGTGGTTCTGTGGAAAATGC
CACGGTGGCTGCCAGACAGCAGCAGTCAAGCCTGGATGGAAAAAAATCCCTTTGTGCTGGGGCAACCTGCA
GGCGGGAGCTGGTGGCTATCCCTACGACCTGGTGGGGCTCCCTGGAAGACGCCAGGAACACCCCCCA
CCCCGATGACCACTGGCTGGCTACGACCTGGTGGGGCTACCTATGCCCTCACACCGCCCTAGACAGCAGGGGAG
GAGGGTGTGCCACACGGAGGACTTCCAGAAGGGAGGGACTGTCAATGGGCTCTGGCACACCGTCGTTG
AAGTCTGAACTGATTCTGACATCCACCAAGAAGTGTATGGTGGTATGACATGGGGCCACAAGGTGTGACTTCAC
ACTTAGCAAAACCAACATGCCAGGATCCGAGAGATCATGGAGAAGTTGGGAAGCAGCCGTCAAGCTGCCAGC
CAGGGCTGAAGCTGCCGGGGCGGAAGAGACGACAGCGTGGTGA
ACCCATGCAAATTAAACCAACCTGGTAGTGTCCATAGTGGACTCACTACTGTTCTCTGTAATTCAAG
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCCAAAAGGGAGGCTGGAGGCTGAGGCTGTTTCTTT
CTTGTTCCCATTTATCCAAATAACTTGACAGAGCAGAGAAAAGCTGATGGAGTGTGAGAGAACCTCAGCAAG
CCAACCTGGGAATCAGAGAGAGAGGAGAAGGGAGGCCCTGGCTCAGAGCCTCTGGCTGCATAGAAAAGG
ATTCTGGTCTCCCTGTTGGCTGGCAGCAAGGGTCCACGTCATTGCAATTGCAAGCTAAATTGCAAG
CATTCCCCAGCTGGCTGCCAAATGTTACCATTTGAGATGCTCCAGGGCTCTAAGAGAACCTCAGGCTC
TGGCCCTGGGACATTGCAAGCTGTCACAAATAATTCTGTTCTTGTGACATAGCCTGCAAGTGCACAT
TCAGTGAGCCTTGAATCTGTTAGTCTCTTTCAACAAAGGAGTGTGTCAGAAAAGGAGAGAGGGCTGA
GATCATTCAAGGAGTTGTTGGCAGCAAGCATGGAGCTTCTTGCAACAAATTCTGGTCCATATAACACCCCCAA
GTCCTGCTGATCCAGTAGCCCTGGAGGTTCCCAGGTAGGGAGGCCAGAGGTGCCAGCCTCTGAAAGGGCCA
GAAAATTAGGCTGGATCTCTTACTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCTGAAGCCCTC
TCTCTGCTTGGAGGTATTGCCCTGTGGAATTGAGTGTCTGATGGGTTGGCTCATATCAGCCTGGAGTTATT
TTGATATGAGAATGCCAGATCTCCAGATTAGGCTAAATGAAAGAACCTCTTAGGATTATCTGTTGAGCAT
CAGTTGGGAAGAATTATTGAAATTCTGCAAGAAAAAAAGTATGTCCTACTTTTGTAAATGTTGCTGCCAT
TGACCTGGAAAAATGAAAAAAATAAGCAATGGTAAGACCCCTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 392

MSRPGTATPALALVLLAVTLAGVGAQGAALEDPDYYGQEWSREPYYARPEPELETFSPPILPA
GPGEEWERRPQEPRPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHSVR
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCAGR
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIFEGNS
EKEIPVLNELPVPVMARYIRINPQSFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTDDLD
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGEHEVGEPEFHYIAGA
HGNEVLGRELLLLVQFVCQEYLARNARIHVHLVEETRIHVLPSSLNPDGYEKAYEGGSELGGWS
LGRWTHDGIDINNNFPDLNTLLWEAEDRNQVPRKVPNHYIAIPEWFLSENATVAAETRAVIW
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYASTHRLMTDARR
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNRR
ESLIVFMEQVHRGIKGLVRDSSHKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKA
EGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRORG

FIGURE 393

GTCCCACATCCTGCTCAACTGGTCAGGCCCTCTAGACCAGCTTGTCCATCATTGCTGAAGTGGACCAAC
 TAGTTCCCAGTAGGGGGCTCCCTGGCAATTCTGATCGCGTTGGACATCTCAGATCGCTTCCAATGAAGA
 TGGCCTGCCTGGGTCTGCTTCTAATCATCTAACATGGGACAAGGTTGCCGGCAGCTCTGGGG
 AAGGAGCACGGGCTGATCAAGGCATCCAGGAACACTGGAGGACTCTGTCAGGCCCTGAAAGAACTCTAGTGGT
 TCTGAATCTAGCCCACCTGGCGTAAGC**ATG**ATGCAACTCTGCAACTCTGCTGGGGCTTGGGCCAGGTGG
 CTACTTATTCTTTAGGGGATTGTCAAGGAGGTGACCCTCTCACGGTCAAATACCAAGTGTCAAGGAGAAGTGC
 ATCTGGTACAGTGTCAAGGAGCTGCCCCAGGAACCTGGCCGGAGGAGAGGGCAGGCAAGCTGGGCCCT
 CCAGGTGTTGAGCTGCCCTAGGCCCTCCATTAGGTGAGCTCTGAGGAAGGCTTGCTCAGCACAGGCAGGC
 GCTGGATCGAGAGCAGCTGCGCACAGTGGATCCCTGCTGGTCTGAGCTGCTGGGCCACAGGGATT
 GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACAGCCACGGTTCCCAAAGGCAGCAGGA
 GCTGAAAATCTCTGAGAGCGCTCTGCGAACCCGATCCCCCTGGACAGAGCTTGTACCCAGACACAGGCC
 TAACACCCTGCACACCTACACTCTGCTCCAGTGAGCACTTGTCCCTGGATGTCATTGTGGGCCCTGATGAGAC
 CAAACATGCAAGAACTCATGGTGAAGGAGCTGGACAGGGAAATCCATTCACTTTGATCTGGTAACTGC
 CTATGACAATGGGAAACCCCCCAAGTCAGGTACAGCTGGTCAAGGTCACAGTCTGGACTCCAATGACAATAG
 CCCTGCGTTGCTGAGAGTTACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAA
 GACCGCCACAGACCTGACCAAGGCCCAATGGGAGGTTGGAGTTCTCAGTAAGCACATGCCCTCAGAGGT
 GCTGGACACCTCAGTATTGATGCAAGACAGGCCAGGTCACTCTGCGTCACCTCTAGACTATGAAAAGAAC
 TGCCCTACGAGGTGGATGTTCAAGCAAGGGACCTGGTCCCAATCTATCCAGCCCATTGCAAAGTCTCATCAA
 GGTTCTGGATGTCATGACAACATCCCAAGCATCCACGTACATGGCCTCCAGCCATCACTGGTGTCAAAG
 TCTTCCAAGGACAGTTTATTGCTCTGTCAATGGCAGATGACTTGGATTCAAGGACACAATGGTTGGTCACTG
 CTGGCTGAGCCAAGAGCTGGCCACTTCAGGCTGAAAAGAACTAATGCCAACACATGTTGCTAACCAATGC
 CACACTGGACAGAGAGCAGTGGCCAAATATAACCTCACTCTGTTAGGCCAACAGGACTCCAGGCCATT
 AGCCAAGAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTGAGAAAAGCAGGTATGA
 AGTCTCCACGGGGAAAACAATTACCCCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
 TAATGAAAAGTCATACCCGATCCAGGACTCCCCAGTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
 GGTCACTGCTCAGAGGTCACTGAACTATGAGAGATGGCCGGTTTGAGTCCAGGTGATGCAAGGACAGCGG
 GCAACCATGCTTGCATCCAGTGTCTGTGGTCAGCCTTGGATGCCATGATAATGCCAGGGTGGT
 CCAGCCTGTGCTAGCAGTGGAAAAGCCAGCCTCCGTGCTGTGAATGCCACAGGCCACCTGCTGGTGC
 CATCGAGACTCCCAATGGCTGGCCAGCAGGGCACTGACACACCTCACTGGCACTCACAGCTCCGGCATT
 CCTTTGACAACCATGTCAGAGATGCAACTCGGGGCAAATGGAGAGGCCCTTACAGCATCCGCAATGG
 AAATGAAGCCCACCTCTTCATCCTCAACCCCTCATACGGGGCAGCTGTCGTCATGTCACCAATGCCAGCAGC
 CATTGGGAGTGAGTGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAAGCCCCCTTACAGACCCGAGCCCTGTT
 GAGGGTCACTGTTGTCACCACTGTGGACCACCTGAGGGACTCAGCCGCAAGCCTGGGCTTGAGCATGTCAT
 GCTGACGGTATGCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCTGGCTTGTTCATGTCATCTGGCG
 GACAGAAAAGAAGGACAACAGGCCCTACAACTGTCGGAGGCCAGTCCACCTACGCCAGGCCAACAGGCC
 CCAGAAACACATTAGCAGAGGAGACATCCACCTCGTGCCTGTGTCAGGGGTCAAGGCAGGTGAGCCTTGTGAAGT
 CGGGCAGTCCCACAAAGATGTGGACAAGGAGGGCATGATGGAAGCAGGCTGGGACCCCTGCTGCAGGCCCTT
 CCACCTCACCCGACCCCTGACAGGACGCTGCTGATACTAACGCAACAGGCCAGGGAGACCCGGAGAGGT
 GCTGCAAGACACGGTCAACCTCTTCAACCATCCAGGCAAGGAAATGCCCTCCGGAGAACCTGAACCTCC
 CGAGCCCCAGCTGCCACAGGCCAGCCACGTTCCAGGCCCTGAGGTTGCAAGGCCAGGCCAACAGGGAGGCTGG
 TGGAGACCAGGGCAGTGAGGAAGGCCCAAGAGGCCACAGCCTCTGCAACCCCTGAGACGGCAGCAGC
 CAATGCCAAAGTGTCCCCCTGAGAAAGAACATAGGCCCTGAGATCCTCTGAGCTGCAACTGCTAGAAGAAG
 GAGCTGTCAGTGTCAAGTGTCTGGACCC
 TGCCTTCGCGAGCGGAACCCCGTGGAGGAGCTCACTGTTGATTCTCTCTGTCAGCAAATCTCCAGCTGCT
 GTCCTTGCTGCATCAGGGCAATTCCAGGCCAACCAAACCAACCGAGGAAATAAGTACTTGGCCAAGGCCAGGAGG
 CAGCAGGAGTGCAATCCAGACAGATGGCCAAGTGCAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
 AGGGCCTTGGATCCTGAAGAGGACCTCTGTAAGCAACTGCTAGAAGAAGAGCTGTCAGTGTCAAGTGTCTGG
 CAGCACAGGTCTGGCCCTGGACCGGCTGAGGCCCTGACCCGGCTGGATGGCGAGACTCTCTTGGCCCTCAC
 CACCAACTACCGTACAATGTGATCTCCCGGATGTCAGGCCACGGAGGCCAGGCCACAGCTTCAGCTCG
 CAAGGCAGAGGCACCAGAGCTGAGGCCAACAGGCACGAGGCCAGCACCTTGTCTGGAGATGAGCTCACT
 GCTGGAGATGCTGTCAGACAGCGCTCAGCATGCCGTGGAGGCCCTCGAGGCCGCTGCGGCCGCTCTGGT
 CTGCGGGAGGACCCCTCAGTTAGACTTGGCCACAGTGCAAGCCTCAGGCATGAAAGTGCAAGGGACCCAGGTGG
 AAAGACGGGGACTGAGGGCAAGAGCAGAGGCCAGCAGCAGCAGCAGCAGGTTGCTG**TGAA**CATACCTCAGACGCC
 CTGGATCCAAGAACCAAGGGCCTGAGGATCTGTGGACAAGAGCTGGTTCTAAATCTGTAACTCACTAGCTAG
 CGGCCGCTGAGAACCTTGGGTGACTGATGCTACCCCAACAGAGGCCAGACAGGCCAGGACTAACAGCTGAC
 TGACCAAAGCAGCCCTTGTAAGCAGCTGAGTCTTGGAGGACAGGGACGGGCTGAGGAGATAAGTGT
 TCCTGGCAAAACATATGTGGAGCACAAGGGTCACTGCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCCAG
 AAAGGGTGGCTTCTGGTAGCAGGAGTCAGGGGCTGTACCCCTGGGGTGCCAGGAAATGCTCTGACCTAT
 CAATAAAGGAAAAGCACTAAAAAAAAAAAAAA

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FIGURE 394

MMQLLQLLLGLGPGGYLFLGDCQEVTTLTVKYQVSEEVPSGTIVGKLSQELGREERRQAG
AAFQLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSDVLATGDLALIHVEIQVL
DINDHQPRFPKGEOLEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGP
ETKHAELIVVKELDREIHSFFDLVLTAYDGNPPKSGTSLVKVNVLDSNDNSPAFAESSLALE
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFSKHMPPEVLDTSIDAKTGQVILRRPLDYEK
PAYEVDVQARDLGPNPPIAHCKVLIKVLVDVNDNIPSIHVWTWASQPSLVSEALPKDSFIALVMA
DDLDSSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS
AKKQLSIQISIDNDNAPVFEKSRYEVSTRENNPLSLHLITIKAHADLGINGKVSYRIQDSPV
AHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDANDNAPEVVQ
PVLSDGKASLSVLVNASTGHLLVPIETPNGLPAGTDTPPLATHSSRPFLTTIVARDADSGA
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPLQTRALLRV
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE
STYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCQLQAPFH
PTLYRTLRNQGNQGAPAESREVQDVTVNLLFNHPRQRNASRENLNLPPEQPATGQPRSRPLKV
AGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE
RNPVEELTVDSPPVQQISQLSLLHQGQFQPKPNHRGNKYLAKPGGSRSAIPDTDGPSARAGG
QTDPEQEEGPLDPEEDLSVKQLLEEELSSLDPSTGLALDRSLAPDPAWMARLSLPLTTNYRD
NVISPDAAATEEPRTFGKAEAPELSPTGTRLASTFVSEMSSLLEMILLEQRSSMPVEAASE
ALRRLSVCGRTLSLDLATSAASGMKVQGDPGGKTGTEGKSRGSSSSRCL

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 395

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGGAGCAGGAGGTGGAGATTCCCAGTTAAAGG
CTCCAGAACCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCACTGGTCCGAATC
AGTAGGTGACCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCGACCTCGTGC
GCCAAGACGTGGATGTTCTGCTCTGCTGGGGGAGCCTGGCAGGCACACTCCAGGGCACAG
GAGGACAAGGTGCTGGGGGTATGAGTGCCAACCCATTGCAGCCTGGCAGGCAGGCCTTG
TTCCAGGGCCAGCAACTACTCTGGCGGTGTCCTGTAGGTGGCAACTGGTCCTACAGCT
GCCCACTGTAAAAACCGAAATACACAGTACGCCTGGAGACCACAGCCTACAGAATAAAGAT
GGCCAGAGCAAGAAATACCTGTGGTTAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT
GTGGAGGACCACAACCATGATCTGATGCTCTTCAACTGCGTGACCAGGCATCCCTGGGTCC
AAAGTGAAGCCCATTGCAGATCATTGCACCCAGCCTGGCAGAAAGTGCACCGTCTCA
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTCTGACACTCTCAACTGTGCAGAAGTA
AAAATTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC
TGTGCAGGCAGCAGCAAAGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGT
GATGGTGCACTCCAGGGCATCACATCCTGGGCTCAGACCCCTGTGGAGGTCCGACAAACCT
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

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FIGURE 396

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV
GGNWVLTAAHCKPKYTVRLGDHSLQNKGDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQL
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP
GQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWI
KKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

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FIGURE 397

GGCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC
TACTGGGCCTGATTGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTGCCGGT
ACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCACCCCCCATCCGAAACGTCACTG
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGCGGCTTCACTGAGAGCTGCA
GCATCTCTCCAAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG
ATAAGTGCCGATGTGCCGTGGCAGCATTGAGTGAGGTGAGGAATGCCCTCCCTGAGC
TCATCGACCTCTACCAGAAATTGGCTTCAAGGTGTTCTCCTCCGGCACCCAGCCATGTGG
TGACAGCCACCTTCCCACACCACCTGTCCATCTGGCTGGCTACCCGCCGTGTCATC
CTGCCTGGACACCTACATCAAGGAGCGGAAGCTGTGCCTATCCTCGGCTGGAGATCTACC
AGGAAGACCAGATCCATTCATGTGCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA
TGAAGGAGACAGAGTGGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCCCTGGCAGCCGG
AGACTTCAGCTGCCACACTGTCACCTGGGCGAGCAGCCGTGGCTGGATGACGGTGACACCC
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGGGCTCCTCTTGAGGAGCTGGACTTGG
AGGGCGAGGGGCCCTAGGGAGTCACGGCTGGACCCCTGGACTGAGCCCTGGGACTACCA
AGTGGCTCTGGAGCCCAGTGCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCCTCC
TGCAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTTCCCTCCT
TCCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGCTCCAGGCCTTGTGCTAAG
CCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCAGGGACTATTTCTGCACCA
GCCCCAGGGCTGCCGCCCTGTTGTCTTTTCAGACTCACAGTGGAGCTCCAGGACC
CAGAATAAAGCCAATGATTACTGTTCACCTGGAAAAAAAAAAAAAAA

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FIGURE 398

MSDLLLGLIGGLTLLLLLTLAFAAGYSGLLAGVEVSAGSPPIRNVTAYKFHMGLYGETGRL
FTESCSISP KLR SIAVYYDNPHMVPDKCRCAVGSILSEGEESP SPELIDLYQKFGFKVFSFP
APSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCP LARQGD
FYVPEMKETEWKWRGLV EAIDTQVDGTGADTMSDTSSVSLEVSPGSRETS AATLSPGASSRGW
DDGDTRSEHSYSES GASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEKGKE

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FIGURE 399

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGGC
TCCGTGCCGCCAAGTTCATTTCACCTCTGCCTCCAGTCCCCAGCCCCCTGGCCGAG
AGAAGGGTCTTACCGGCCGGATTGCTGGAAACACCAAGAGGTGGTTTGTTTTAAA
ACTCTGTTCTGGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCTGCTCTGTTTC
TGGAGCCTCTGCTATTGCTTGCTGCAGGGGAGCCCCGTACCTTGGTCCAGAGGGACGGCTG
GAAGATAAGCTCCACAAACCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGGTTAAC
CTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAGCCAGCCC
TTAGAAGACTGCAGTTCAACATGACAGCTAAACCTTTCATCATTACGGATGGACGATG
AGCGGTATCTTGAAAAGCTGGCTGCACAAACTCGTGTCAAGCCCTGCACACAAGAGAGAAAGAC
GCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTACACGGATGCGGTCAAT
AATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTGACTGGCTGCAGGAGAAGGACGAT
TTTCTCTCGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTGGCCGGTATGCA
GGCAACTCGTGAAGGAACGGTGGGCCAATCACAGGTTGGATCCTGCCGGCCATGTT
GAAGGGGCCACATCCACAAGAGGCTCTCCGGACGATGCAGATTGTGGATGTCCTCCAC
ACCTACACGCCTCCTCGGCTTGAGCATGGTATTAGATGCCTGTGGCCACATTGACATC
TACCCCAATGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGTCTGGATCAATTGCA
TATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCGTCCACCTCTTGTGAC
TCTCTGGTGAATCAGGACAAGCCGAGTTGCCTCCAGTGCAGTCCAATCGCTTCAAA
AAGGGGATCTGTCTGAGCTGCCCAAGAACCGTTGTAATAGCATTGGCTACAATGCCAAGAAA
ATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGGCAGGCATGCCCTTCAGAGGT
AACCTCAGTCCTGGAGTGTCCTGAGGAAGGCCCTTAATACCTCCTTTAACCATGCT
GCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCACAATCAAATCGTTGCAA
ATCAGATTACACTGTGCATGTCCTAGGAAAGGAATCTTACAAAATAAACAGTGTGGACCC
TAATAA

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FIGURE 400

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFLRTSKDPEHEG
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWLPL
AHQLYTDAVNNTRVVGHSIARMLDWLQEKKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI
TGLDPAGPMFEGADIHKRSLPDDADFDVLHTYTRSFGLSIGIQMPVGHIDIPNGGDFQPGC
GLNDVLGSIAYGTTIEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLSCRKNR
CNSIGYNAAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 401

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATGCCTGCAGAACTTCTACTTGCGCTG
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTCCTCTGATGGGGACCTCCTGT
CAGTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGCTTCCCAGGCCAAGTGGCTC
AACTCTCCTGCACGCTCAGCCCCAGCACGTACCACATCAGGGACTACGGTGTGCCTGGTACC
AGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCTGTGTCC
TCACCATTAGTCCC GTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT
TTAGTCCCTAGGGTGGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCATTCTGCCCTGA
CCTTGGGTCCCTTTAAACTTCTCTGAGCCTGCTTCCCCTGTAAAATGGGTTAATAATA
TTCAACATGTCAACAAAC

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FIGURE 402

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCSVGYGFSP

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FIGURE 403

CGCGCCGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG
GCAGAGCAGGGCTGCATTCAGCAGGAGCTGCGAGCACAGTGTGGCTACAACAAGATGCTCAAGGTGTCAGC
CGTACTGTGTGTGCAGCCGTTGGTGCAGTCAGTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGG
GCGGTCGGACGGCGTAATTCTGGATGATAAACAAATGGCTACCACAAATCTCAGTATGACAAGGAAGTCGG
ACAGTGGAACAAATTCCGAGACGAAGTAGAGGATGATTATTCGCACTGGAGTCCAGGAAAACCTTCGATCA
GGCTTAGATCCAGCTAAGGATCCATGCTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATT
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG
GAGGGGTCCTCATATTATCCACCTGCAAGCAGTGCCTAGGGTCTATCCCAGCCCTGTTGTGGTCAGATGGTC
TACCTACTCTTCAGTGCAAACACTAGAATATCAGGCATGTGCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG
ACATTGCCATGTCCTTCAGATAAGCCCACCAAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT
CAGGGAAAGTGGCAAACAGATTGCGGGACTGGTCAAGGCCCTCATGAAAGTGGAAAGTCAAAACAAGAACAAA
AACATTGCTGAGGCCTGAGAGAACAGATTGATACCAGCATCTGCCAATTGCAAGGACTCACTGGCTGGAT
GTTAACAGACTTGATACAAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAACGACTTACCTTGATAAGAA
TGAACAGTGTACCAAGGCATTCTCAATTCTTGACACATACAAGGACAGTTAATATCTAATAATGAGTGGTG
CTACTGCTCCAGAGACAGCAAGACCCACCTGCCAGACTGAGCTCAGCAATATTCAAGCGGCAAGGGTAAA
GAAGCTCCTAGGACAGTATATCCCCCTGTTGATGAAAGATGGTACTACAAGCCAACACAATGTCATGGCAGTGT
TGGACAGTGTGGTGTGACAGATATGAAATGAAAGTCACTGGGATCCAGAATAATGGTGTGAGATTGTG
TATAGATTTGAGATCTCGGAGATTTGCTAGTGGCGATTTCATGAATGGACTGATGATGAGGATGATGAAGA
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGA
CCATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAAATTCTACATTCTAATATTACAAAAATGATAG
CCTATTAAAATTATCTCTCCCCAATAACAAAATGATTCTAACCTCACATATATTGTATAATTATTGAA
AAATTGAGCTAAAGTTAGAACCTTATGTTAAATAAGAATCATTGCTTGAGTTTATATTCTTACACA
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTGAAGTGTACTATAAAATTTCACGAGA
ACAAACTTGTAAATCTTCCATAAGCAAAATGACAGCTAGTGCTGGGATCGTACATGTTAATTGGTAAAGAT
AATTCTAAGTGAATTTAAAATAAAATTGTTAATGACCTGGTCTTAAGGATTAGGAAAATATGCATGCT
TTAATTGCATTCCAAAGTAGCATCTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA
AAAAAAAAAAAAAA

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FIGURE 404

MLKVS A V L C V C A A A W C S Q S L A A A A A V A A A G G R S D G G N F L D D K Q W L T T I S Q Y D K E V G Q W N K F R D
E V E D D Y F R T W S P G K P F D Q A L D P A K D P C L K M K C S R H K V C I A Q D S Q T A V C I S H R R L T H R M K E A G V
D H R Q W R G P I L S T C K Q C P V V Y P S P V C G S D G H T Y S F Q C K L E Y Q A C V L G K Q I S V K C E G H C P C P S D K
P T S T S R N V K R A C S D L E F R E V A N R L R D W F K A L H E S G S Q N K K T K T L L R P E R S R F D T S I L P I C K D S
. L G W M F N R L D T N Y D L L D Q S E L R S I Y L D K N E Q C T K A F F N S C D T Y K D S L I S N N E W C Y C F Q R Q Q D P
P C Q T E L S N I Q K R Q G V K K L L G Q Y I P L C D E D G Y Y K P T Q C H G S V G Q C W C V D R Y G N E V M G S R I N G V A
D C A I D F E I S G D F A S G D F H E W T D D E D D E D D I M N D E D E I E D D D E D E G D D D D G G D D H D V Y I

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

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FIGURE 405

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FIGURE 406

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCQRNQTHRSSLHYKPTPDLRISIENSEE
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLSDKASSLLCFQHQE
ESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSSPPHTAAHNASVDMCELKRLDQLLSQF
LKHPQKASRRPSAAPASQQLQSLQSKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH
SRQEEEQSEIMEYSVLLPRTLFQRTKGRSGAEKRLLLVDFSSQALFQDKNSSQVLGEKVLCI
VVQNTKVANLTEPVVLTQHQQLQPKNVTLQCVFWEDPTLSSPGHSSAGCETVRRETQTSCF
CNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPPLCRRKPRDY
TIKVHMNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLV
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS
LVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLLGLSLVLGLPWALIFFSF
ASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

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FIGURE 407

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCAGGGGTGGCAGGAG
CCGCAGAGCCAGAGCAGACAGCCGAGAACAGGTGGACAGTGTGAAAGAACCAAGTGGTCTCGC
TCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTACTGCAGCCTCAGACTCCTGGA
CTTGAGAAATCCTCCTGCCCTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC
TGTTTCTTCTCCTTCTGTGAGTGGACCCACGGAGGCTGGTGAGCTGCCCTGTCACTCCAAAGCTC
AGCTCTGAGCCAGAGTGGTGGCTCCACCTCTGCCGCCGATAGAACGCCAGGAGCAGGGC
TCTCAGAAGGCCGGTGGTGCCAGCTGGGAT**CATGTTGTTGGCCCTGGTCTGCTCAGCTG**
CCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACGGCAGAGTGCTACATGA
CTTCGGGCTGGACGGATAACGGGATACAGCCTGGCTGACTGGGCTGCCCTGCTTATTAC
AAGCGGTTCAACGCAGCTGCTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAACGTGTGCCGGAT
GTACTGCTCAGATTGTTGAATCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC
CCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT
CACTGAATGGGTGGATGGCTGTGACTTC**TAGGATGGACGGAACCATGCACAGCAGGCTGGGAA**
ATGTGGTTGGTCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG
TGAAA

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FIGURE 408

MLLALVCLLSCLLPSSREAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAALDY
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPMQGLGYWE
AWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 409

CAGACTCCAGATTCCCTGTCACCACGGAGTCCAGAGAGGAACGGAGCGGAGACAACAGTACCTGACGC
CTCTTCAGCCGGGATCGCCCCAGCAGGGATGGCGACAAGATCTGGCTGCCCTCCCGTGCCTCCTCTGGCC
GCTCTGCCTCCGGTCTGCTGCCCTGGGCGGCCGCTCACACCTTCCCTCGATAGCGACTTCACCTTACCCCT
CCCGCCGGCCAGAAGGAGTGCTCTACCAAGGCCATGCCCTGAAGGCCTCGAGGATCGAGTACCAAGTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTGAAACAAAGAAAA
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTATTACATGTTCTGCTTGACAATACATTAGCACCATT
TCTGAGAAGGTGATTTCTTGAATTAATCTGGATAATATGGGAGAACGGCACAAGAACAGAAGATTGAAAG
AAATATATTACTGCCACAGATATATTGGATATGAAACTGGAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTGAGCTCGTGCATCGAAACATACAAGAAC
AACTTGTAGAGTCATTTCTGGTCTATGGTTAATTAGTGTGTCATGGTGTGTCAGCCATTCAAGTTAT
ATGCTGAAGAGTCGTTGAAGATAAGAGGAAAGTAGAAACTAAAACCTAGAGTACGTAACTTGAA
AATGAGGCATAAAATGCAATAAAACTGTTACAGTCAGACCATTATGGTCTCTCCAAAATATTGAGATATA
AAAGTAGGAAACAGGTATAATTAAATGTGAAAATTAAAGTCTTCACTTCTGCAAGTAATCTGCTGATCCAG
TTGACTTAAGTGTGAAACAGGAATTTCAGTGTAACTATTGAGAAAGCATTAGTCTTGTACTTGCTTACATTC
TTCTCAACTTGAAAATTGCAAATGTTAGGTGATTAAATAATGAGTATTGGCCTAATTGCAACACC
AGTCTGTTAACAGGTTCTATTACCCAGAACTTTTGTAATGCGGAGTTACACTTAAATTAGGACATGTTCTTGT
TCAGTTAACGTTAAATCACCTGAGAATTACCTAATGATGGATTGAAATAATCTTAGACTACAAAAGCCAA
CTTTCTCTATTACATATGCATCTCCTATAATGAAATTAGAATAATAGCTTGAATAACATTAGGTTTTG
AGATTTTATAACCAAATACATTTCAGTGTAACTATTGAGAAAGCATTAGTCTTGTACTTGCTTACATTC
CCAAAGCTGACATTTCACGATTCTTAAACACAAAGTTACACTTAAATTAGGACATGTTCTTGT
AAATGAAAGAATATAGTTAAAGCTTCCCTCCATAGGGACACATTCTCAACCTTAACAAAGTGTAGGA
TTTAAATTAAATGTGAGGTTAAATAAGTTATTAAATAGTATCTGCAAGTTAAATCTGCAACAGTTAA
TAATCATGTTATGTTAATTAAACATGATTGCTGACTTGGATAATTCTTACCGCAGTTAGGAAGGAAATA
TTGCTAAATGATCTGGCCTACCATAAAATAAATCTCCTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
AGAATTAGAAAACCTGAGGAAACCTAACTCCAAATAAAACTTCACTTAAGTAGAAACTAAATAATCTAGA
ATCTGACTGGCTCATGACATCCTACTCATAAACATAATCAGGAGATGATTAACTTCCAGTTAGCTGGAAG
AAACTTGGCTGAGGTTTATTCTACAAGAACTTAAATTGGGTATAGAACCCCTAACAGGTTAGTAATGCTGGAATT
AAATGTAAGCCCTACTGTAAGGTTAGCACTGGGTGACATATTATAAAATTATTATAACAACATT
TAAAATGCCCTTCTGAAACACTTATTATTGATGTTGAAGTAGGATTAGAAACATAGACTCCAAAGTTAA
CACCTAAATGTGAATAACCCATATACAACAAAGTTCTGCATCTAGCTTTGAAGTCTATGGGGTCTTAC
TCAAGTACTAGTAATTAACTTCATGAACTGAACTATAATTAAAGTTATGCCATTATAACGTTGTTAT
GACTACATTGTGAGTTAGAAACAAACTTAAATTGGGTATAGAACCCCTAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAAGAGAGTGATTCACTCATAGTAGTATAAAAGAGATACTTCCC
TCTTAGGCCCTGGGAGAAGAGCAGCTAGATTCCCTACTGCCAAGGTTAAATGAGTAAATGCCGTAT
ATGATCAATTACCTTAATTGCCAAGAAAATGCTTCAGGTGCTAGGGTATCCTGCAACACTGAGAACAA
AGGTCAATAAGATCCTGCCTATGAATACCCCTCCCTTTGCCTGTTAAATTGCAATGAGAACAAATTACA
GTACCATATAAAAGCAGGGTACAGATATAAAACTACTGCACTTCTATAAAACTGTGATTAGAATTCTA
CCTCTCTGTATGGCTGTTACTGTAAGTCTGACTCCCTACCTAACAAATGAAATTGTTACATAATCTCT
ACATGTATGATTGTCACGTGATCTAAACCTATGATTGAGCTAACCTTCTACCATATAAAACGATAATTGCTT
TATTGGAAAAGAATTAGGAATACTAAGGACAATTATTGTTAGACAAAGTAAAAGACAGATATTAAAGAGG
CATACCAAAAGCAGGAAACTTGAAACAGAGTAAATTCTAAATTGCTAAATTGAGTAAAGCTGTTTAC
CATATGCTTTTAAATTCACTATTCCATTCTAAATTAAAGTTGCTAAATTGAGTAAAGCTGTTTAC
AACAGCTATTGCTTTCAATACAAATTAAAGTACTACAAATTGCTAAAGGCCAACGATTTC
CATAATGTAAGCAGTTACCGTGTTCACCTCACACTAACGGCTAGAGTTGCTGATATGCAATTGGATGATTAA
GTTATGCTGTTCTTCAATGTAAGACATGGAGGGTGTGTAATTGTTATGGAAAATTAAATCCTCTTA
CACATAATGGTGTCTTAAATTGACAAAAATGAGCACTTACAATTGTTGCTCCTCAAATGAAAGATTCTTAT
GTGAAATTAAAGACATTGATTCCGCATGTAAGGATTTCATCTGAACTACAATAATGCAACAGTATTGAGTACTGATATGATATAAA
AAATTATCAAAGGAAAA

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FIGURE 410

MGDKIWLPFPVLLAALPPVLLPGAAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEYQ
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFELIL
DNMGEQAQEQQEDWKKYITGTDILDLMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE
SNFDRVNFWSMVNLVVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 411

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FIGURE 412

MVGTKAWVFSFLVLEVTSQLGRQTMLTQSRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID
YPGGKGDYERLDAIRFYGYDRVCARPLRLEARDDWTAGSTGQVVHGSREGFWCLNREQRP
GQNCSNYTVRFLCPPGLRRDTERIWSWPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAWSLPGGAPASGAIIYLLTTPKL
LTQTDSDGRFRIPGLCPDGKSILKITKVFKAPIVLTMPKTSIKAATIKAEFVRAETPYMVNP
ETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAGEYFCKA
QSDAGAVKSKVAQLIVTASDETPCNPVPESYLIIRLPHDCFQNATNSFYDVGRCPVKTCAGQQ
DNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP
MRFGHVYMGNSRVSMGYKGTFTLHVPQDTERLVLTFVDRLQKFVNNTKVLPFNKKGSASFHE
IKMLRRKEPITLEAMETNIIPLGEGVVEDPMAELEIPSRSFYRQNGEPYIGKVKASVTFLDPR
NISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTESEPLNAGKVKVHLDSTQVKMPEHI
STVKLWSLNPDGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNLDPESRRCFVKV
RAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSSITGPNGACVPACDDQSPDA
YSAYVLASLAGEELQAVESSPKFNPNNAIGVPQPYLNKLYRRTDHEDPRVKKTAQFQISMAKPR
PNSAEESENGLYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFNEDDPMSTEDYLAWW
PKPMEFRACYIKVKGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF
KCSGMLYDQDRVDRTLVKVIPQGSCRRASVNPMLEYLVNHLPLAVNNDTSEYMLAPLDLG
HNYGIYTVDQDPRTAKEIALGRCFDGTSGSSRIMKSNVGVALTFNCVERQVGRQSAFQYLO
STPAQSPAAGTVQGRVPSRRQQASRGGRQGGVVASLRFPRAQQPLIN

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FIGURE 413

GCCACGTTGTCTTCTTCCTTACCAACCACCCAGGAGCTCAGAGATCTAAGCTGTTCCATC
TTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCTCTTGCCCTCCTCTC
ATCCTAATCCCCCTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTCCCTAGACTCCGTT
ATGGATAAGAAGATCAAGGATGTTCTAACAGTCTAGAGTACAGTCCCTCCTATAAGCAAG
AAGCTCTCGTGTGCTAGTGTAAAAGCCAAGGCAGACCGTCCTGCCCTGCTGGATGGCT
GTCACTGGCTGTGCTTGTGGCTATGGCTGTGGTTGTGGATGTTCAGCTGGAAACCACCTGC
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCGCTGCTGCCACCTGACTGACAGGGA
GGAGGCTGAGAACTCAGTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCCCTGATTCTGGTAATAAGACAAACTTT
GTACCTCAAAAAAAAAAAAAAAA

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FIGURE 414

MGPSSCLLILIPLLQLINPGSTQCSLDSDVMDKKIKDVLSLEYSPSPISKLSCASVKS
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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FIGURE 415

CAGAAGAGGGGGCTAGCTAGCTGTCTCGCGACCAGGGAGACCCCCGCGCCCCCGGTGTG
AGGC GG CCTCACAGGGCCGGGTGGCTGGCGAGCCGACGCCGGCGGGAGGAGGCTGTGAGGA
GTGTGTGGAACAGGACCCGGACAGAGGAACCATGCTCCGCAGAACCTGAGCACCTTGCC
TGTTGCTGCTATAACCTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTGGGGG
TGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCATAGGAAACTAGCCCTGCAGCTTC
ATCCCGACCAGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTT
ATGAGGTTCTGTCAGATAGTGAGAACGGAAACAGTACGATACTTATGGTAAGAAGGATTAA
AAGATGGTCATCAGAGCTCCCATGGAGACATTTCACACTTCTTGGGATTGGTTCA
TGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAAAGAGGAAGTGAATTATTGTAG
ATCTAGAAGTCACTTGGAAGAAGTATATGCAGGAAATTGTGGAAGTAGTTAGAAACAAAC
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGATGCGGACCACCC
AGCTGGGCCCTGGCGCTTCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGTGAGAGACGGCATGG
AGTACCCCTTATTGGAGAACGGTGAGCCTACGTGGATGGGAGCCTGGAGATTACGGTCC
GAATCAAAGTTGTCAAGCACCAATATTGAAAGGAGAGGAGATGATTGTACACAAATGTGA
CAATCTCATTAGTTGAGTCACTGGTTGGCTTGAGATGGATATTACTCACTGGATGGTCACA
AGGTACATATTCCGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG
GGCTCCCCAACTTGACAACAACATATCAAGGGCTTTGATAATCATTGATGTGGATT
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAACGGTATCAAACAGCTACTGAAACAAGGGT
CAGTGCAGAACGGTATACAATGGACTGCAAGGATATTTGAAGGTGAATAAAATTGGACTTGT
AAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTTGTGTGTTTGT
TTTCAATATGCAAGTTAGGCTTAATTGGCTTATCTAATGATCATGAAATGAATAAGAGG
GCTTAAGAATTGTCCATTGCAATTGCGAAAGAATGACCAGCAAAAGGTTACTAATACCTC
TCCCTTGGGATTAAATGTCTGGTGTGCCGCTGAGTTCAAGAATTAAAGCTGCAAGAGG
ACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGTTGTAGCAATTCAAAATG
CCAACGGAGAACAGTCTGTTTAAATACATTGTTATTGTTA

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FIGURE 416

MAPQNLSFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQL...AAYE
VLSDSEKRKQYDTYGEEGLKDGHQSSHGDIIFSHFFGDFGMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNF
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFI
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLW
KKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEARREGIKQLLKQGSVQKVYNGLQGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 417

CGGCGGCGGCTCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGGA
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAAGTGAAGAGGCCGGAGAGGGCCCAGCCCAGGGCAG
GATGACCAAGGCCCGCTGTTCCGGCTGTGGCTGGCTGGTCACTGATCCTGCT
GATCATCGTGTACTGGGACAGCGCAGGCCGCCACTTCTACTTGACACGTCCTTCTCTAG
GCCGCACACGGGGCCGCGCTGCCACGCCGGGCGACAGGGACAGGGAGCTCACGGCCGA
CTCCGATGTCGACGAGTTCTGGACAAGTTCTAGTGTGGCGTAAGCAGAGCGACCTTCC
CAGAAAGGAGACGGAGCAGCCGCTGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA
CTGGTCCCCCGCGACGCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGAGCGGAGGAG
CGTGCTGCAGGGCTTCTGCGCCAACCTCCAGCCTGCCCTCCCCACCAAGGAGCGCGATTGCA
CGACATCCCCAACCTGGAGCTGAGCCACCTGATCGTGGACGACCGGACGGGCATCTACTG
CTACGTGCCAACGGTGGCCTGCGCCAACCTGGAAAGCGCGTGTGATCGTGTGAGCGGAAGCCT
GCTGCACCGCGGTGCCCTACCGCGACCCGCTGCCATCCCGCGAGCACGTGACAACGC
CAGCGCGCACCTGACCTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCGCCACCTCAT
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCGTGCAGCCGACCCCTTGTGCGCCTGAT
CTCCGCCTCCGCAGCAAGTTGAGCTGGAGAACGGAGGAGTCTACCGCAAGTTGCCGTGCC
CATGCTGCCGTGTACGCCAACACACCAGCCTGCCCTGGCGCGAGGCCCTCCGCC
TGGCCTCAAGGTGTCCCTGCCAACCTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT
GGCGCCCTCAACGAGCACTGGCGCAGGTGTACCGCCTTGCCACCCGTGCCAGATGACTA
CGACTTCGTGGGAAGCTGGAGACTCTGGACGAGGACGCCGCCAGCTGCTGCAGCTACTCCA
GGTGGACCGGCAGCTCCGCTCCCGAGCTACCGGAACAGGGACGCCAGCAGCTGGGAGGA
GGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA
CTTGTTCTTCGGCTACCCCAAGCCGAAAACCTCCGAGACT**GA**AAGCTTCGCGTTG
CTTTTCTCGCGTGCCTGGAACCTGACGCCAGCGCACTCCAGTTTTATGACCTACGATT
TGCAATCTGGCTTCTGTCCTCCACTGCCCTATCCATTGAGTACTGTATCGATATTGTT
TTTAAGATTAATATATTCAGGTATTAATACGA

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FIGURE 418

MTKARLFRLWLVLSVFMILLIIVYWDSAGAAHFYLHTSFSRPTHGPPLPTPGPDRDRELTAD
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS
VLRGFCANSSIAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSL
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLRSRHLMKVKKLYTKFLVRDPFVRLI
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL
APFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRTASSWE
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 419

GGCACGAGGCTGAACCCAGCCGGCTCATCTCAGCTCTGGTTCTAAGTCATGTGCCAAAG
GCTGCCAGGAAGGAGACGCCTCCTGAGTCCTGGATCTTCTCCTCTGGAAATCTTGACT
GTGGGTAGTTATTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA
AGTCTCAGTCCTGTGCCACCTGGTCTCTGCTACGTCTTATTGCCTCAGGGCTAACATCA
ACACCATTCACTCTTCACTCTCCTCTGGCCATTAAACAAGCAGCTCTCCGGAAAGATCA
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTATGCTGCTGGAGTGGTGGCGA
CGGAATGCACCATTTCACGGACCCGCGCGCTACCTCAAGTATGGAAAGGAAATGCCATCG
TGGTCTCAACCACAAGTTGAAATTGACTTCTGTGTGGCTGGAGCTGTCCGAACGTTTG
GGCTGTTAGGGGCTCAAGGTCTGGCCAAGAAAGAGCTGGCTATGTCCAATTATCGGCT
GGATGTGGTACTTCACCGAGATGGTCTTCTGTCGCGCAAGTGGAGCAGGATCGCAAGACGG
TTGCCACCAGTTGCAGCACCTCCGGACTACCCCGAGAAGTATTTTCCTGATTCACTGTG
AGGGCACACGGTTCACGGAGAAGAACATGAGATCAGCATGCAAGGTGGCCCGGGCCAAGGGGC
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTCGCCATCACCGTGAGGAGCT
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAAGAAATAATGAAAATCAA
CACTGCTGGAGTCCTAACGGAAAGAAATACCATGCAAGATTGTATGTTAGGAGGATCCCAC
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCTGGCTGCACAAGCTTACCAAGGAGA
AGGATGCCTTCAGGAGGAGTACTACAGGACGGCACCTCCAGAGACGCCATGGTCCCC
CCGGCGGCCCTGGACCCCTGTAAGTGGCTGTTTGGGCTCGTGGTGTCTACCCCTTCT
TCCAGTTCTGGTCAGCATGATCAGGAGCGGTCTCCCTGACGCTGGCAGCTTCATCCTCG
TCTTCTTGTGGCTCCGTGGAGTTGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT
CTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACTCAGGGAGGTGTCACCAT
CCGAAGGGAACCTGGGAACGGTGGCCTCTGCATATCCTCCTAGTGGACACGGTGACAA
AGGCTGGGTGAGCCCTGCTGGCACGGCGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT
CTCAAGGCCGGATGGGAGGAAGATGTTGTAATCTTTTCCCCATGTGCTTTAGTGGG
TTGGTTTCTTTGTGCGAGTGTGTGAGAATGGCTGTGGTGGAGTGTGAACTTGTT
TGTGATCATAGAAAGGTATTTAGGCTGCAGGGAGGGCAGGGCTGGGACCGAAGGGGACA
AGTTCCCCTTCATCCTTGGTGTGAGTTCTGTAACCTGGTTGCCAGAGATAAAAGTGA
AAAGTGCTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAATTAAAGTGCTTTCT
GGTCAAAAAAAAAAA

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FIGURE 420

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLGGSKVLAKKEL
AYVPIIGWMWYFTEMVFCRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHEISM
QVARAKGLPRLKHLLPRTKGFAITVRSLRNVSAVDCTLNFRNNENPTLLGVNLNGKKYHAD
LYVRRIPLEDIPEDDDECASAWLHKLYQEKFQEEYYRTGFPETPMVPPRRPWTLVNWLFWA
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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FIGURE 421

CGGACGCGTGGCGGACCGTGGCGGACCGTGGCGGACCGTGGCTGGTGCCTGCATC
GCCATGGACACCACCAGGTACAGCAAGTGGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTTTCTTGGCCCTGGCTGTCTGGTCACC
ACAGTCCTTGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCG
CTGCTTGACGCCACGACCTGCTGAGGACAAACGCCCTGAAGCAGACGGCGCTGGGTGCC
CTGAAGGAGGAGGTGGAGACTGCCACAGCTGCTGGGGACGCAGGCCAGCTGCAGACC
ACGCCGCGGGAGCTGGGAGGCCAGGCAGCTGATGGAGCAGGAGAGGCCCTGCCGGAA
CTGCGTGAGCGCGTGACCAGGGCTTGGCTGAAGCCGGCAGGGCCGTGAGGACGTCCGC
GAGCTGTTCCGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCGTGCC
TCGTGGCTGTCCTCGAGGGCTCTGCTACTTTCTGTGCCAAAGACGACGTGGCG
GCCAGGATCACTGCGCAGATGCCAGCGCACCTGGTGATCGTTGGGGCTGGATGAGCAG
GGCTCCTCACTCGAACACCGTGGCGTGGTACTGGCTGGCCCTGAGGGCTGTGCC
CTGGGCAAGGTTAGGGTACCAAGTGGTGGACGGAGTCTCTCAGCTCAGCCACTGGAAC
CAGGGAGAGCCAATGACGCTGGGGCGCGAGAACTGTGTATGATGCTGCACACGGGCTG
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACA
TGACCCCGCCAGTGCCCTGGAGGCCGCCATTGCAGCATGTCGTATCCTGGGGCTGCTCA
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTCTTCATCCACCGCTGCTGAG
TCTCAGAAACACTTGGCCAACATAGCCCTGTCCAGCCAGTGCCTGGCTCTGGACCTCCA
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACCTCCACTAGCTCAA
CTGCTCCTGCGTCCCCGTGATATGCCCTCACTTCTCCCTAACCAAGGTTAGGTGACTGAGG
ACTGGAGCTTTGGTTCTCGCATTTCCACCAAACGGAGCTGTTTGAGCCTGAGG
AAGCATCAATAAATATTGAGAAATGAAAAAA

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FIGURE 422

MDTTRYSKWGSSEEVPGPWVHWSRRPLFLALAVLVTTLWAVILSILLSKASTERAAL
LDGHDLRLTNASKQTAALGALKEEVGDCSCHSCSGTQAQLQTTRAELGEAQAKLMEQESALREL
RERVTQGLAEAGRGRVEDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFHWNQ
GEPNDAWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 423

GGCCGCCAGCGTAGGCAGGGTGGCCCTGCGTCTCCGTTCTGAAACCCGGCGGGC
GAGCGAGGCTGCGGGCCGGCGCTGCCCTCCCCACACTCCCCCGAGAACGCTCGCTCGC
GCCAACATGGCAGGGTGGCGCTGCCGCCAGCTAACGGCGCTCTGCCGCTGGATCGC
GGCTGTGGCGGCAGGCCAGGCCAGGAGGCCGCTGCCGCCAGCAGAGCCGGTCCA
GCCCATGACCGCTCCAAGTGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTACGC
CCCATGGTGCCATCTGCCAGCAGACTGATTCAAATGGAGGCTTGTCAAAGAATGGTGA
AATACTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAAGAACAGGTTGAGTGGCGCTT
CTTGTCAACACTCTCCAGCATTTCATGCAAAGGATGGGATATTCCGCCATTACGTGG
CCCAGGAATCTCGAACGACTGAGAATTATATCTAGAGAAGAAATGGCAATCAGTCAGGCC
TCTGACTGGCTGGAAATCCCCAGCTCTAACGATGTCTGGAAATGGCTGGTCTTTAGCAT
CTCTGGCAAGATATGGCATCTCACAACTATTCACAGTGAECTTGGAAATTCTGCTGGT
TTCTTATGTGTTTCGTCAAGGCCACTGGTTTGGCCTTTATGGGCTGGTCTGAGCAGAA
GGTAATATCAGAATGTTCTATGTGCCACTTCAAGGCATTATCTGAGCAGGTTCTGAGCAGAA
TCGGAGATCAGAGGAGGCTAGAGCTAACAGCTTGCAAGGATGCCAGGAGGAGGAAAAAGATGA
TTCAAATGAAGAAGAAAACAAAGACAGCCTGTAGATGATGAAGAAGAGAAAGATCTGG
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGACAACCTGGCTGTGGATGAGGA
GAGAAGTGGGCCATGATCAGGGGCCAGGAGAGGACGGTGTGACCCGGAGGAAGTGA
GCCTGAGGAGGCTGAAGAAGCATCTGAGCAACCTGCCAGCTGACACAGAGGTGGTGA
AGACTCCTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGACTGTAGTTAATGATGCGT
TTCAAGAATACACACAAAATATGTCAGCTCCCTTGGCCTGCAGTTGTACCAAATC
CTTAATTTCCTGAATGAGCAAGCTCTTAAAGATGCTCTAGTCATTGGTCTCATG
GCAGTAAGCCTCATGTATACTAAGGAGACTTCCAGGTGTGACAATCAGGATATAAGAAAAC
AAACGTAGTGTGGGATCTGTTGGAGACTGGATGGAACAAGTCATTACTTAGGGTCA
GAGAGTCTGACCAGAGGAGGCCATTCCAGCTTAATCAGCACCTCCAGAGACAAGGCTGC
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTGGCTCTGAGCATCCCCAAAGTGTAAAGT
AGAACGCTTCGCATCCTTCTTGTAAAGTATTATTTGTCAAATTGCAAGGAACATCAG
GCACCACAGTCATGAAAGGAAATCTTCACAGCTAGAAATTGAAAGGGCTGGGTATAGAGAGC
AGACTCAGAAGTCATCCAGCCCTGTGAAATCTCTGTGCTATGTTTATTCTACCTTAATT
TTTCCAGCATTTCCACCATGGCATTGGCCTCTGAGCTCCACACTCTTCACTATTATCTCTGGTCA
GAGGACTCCAATAACAGCCAGGTTACATGAAGCTGTGACTGCCAACATCTCAAATGAAATGTTGT
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAACATCTCAAATGAAATGTTGT
GCCATCAGAGACTAAAAGGAAGTAAGGATTTACAAGACAGATTTTTGTTTGTGAAAG
CCAAAATATAGTTGTGTTGATTTTTAAGTTCTAAGCAATATTTCAGGCCAGAAG
TCCTCTAAGTCTGCCAGTACAAGGTAGCTGTGAAAGAAAAGTGAATACTGTTTGTGTTTC
ATCTCAAGGGGTTCCCTGGGTCTTGAACTACTTAAATAACTAAAAAACCACTTCTGATTT
TCCTTCAGTGTGCTTTGGTGAAGAATTAAATGAACCTCAGTACCTGAAAGTGAAGATT
TGATTTGTTCCATCTCTGTAAATCTTCAAAGAATTATATCTTGTAAATCTCTCAAAACT
CAATCTACTGTAAGTACCCAGGGAGGCTAATTCTTT

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FIGURE 424

MAGGRCGPQLTALLAAWIAAVAAATAGPEEAALPPEQSRVQPMTASNWTLMEGEMLKFYAPW
CPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRGPG
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNFTVTLGIPAWCSY
VFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEKDDSN
EENKDSLVDDEEEKEDLGDEDEAEEEEEDNLAAVGDEERSEANDQGPPGEDGVTRREEVEPE
EAEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide

isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 425

GAGGAACCTACCGTACCGCCGCGCTGGTAGTCGCCGTGCGCCTCACCAATCCGTGCGCCGCG
 CTGGGCCGTGGAGAGTCGTGCTCTCTCCTGCACGCCGTGCTGGCCTCGGCCAGGCCGGGTCCGCCGCA
 GGGTTTGAGGATGGGGAGTAGCTACAGGAAGCAGCCCGCGATGGCAAGGTATATTTGTGGAATGAAAAGGA
 AGTATTAGAAATGACCTGAAGACCATTACAGATAAATATTGGCATATTACACTGAACTGGACAGCAGTGAATCTAACCT
 TGAAGTAATGTAGACAGAAAGTCTCAAATTGCAATTACACTGAACTGGACAGCAGTGAATCTAACCT
 TAAATCAGAAACTTGCATAAGAAAGAGAATGGGAGTGGTAATTGGGACAGATTGTGATGCTTGATTCAC
 GATCATTCTCTGTTCTGATAGTGTATATGCCATTAGGGACAGATCAGGATTTCAGTTACAGTTACTTGG
 AGTGTCCAAAATGCAAGCAGTAGAGAAAATAGACAAGCTTCAGAAATTGGCATTGAAGTTACATCCTGATAA
 AAACCGAATAACCCAAATGCCATGGGATTTTAAAAATAATAGACATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAAAGTATGCAAAATATGGAGAAAGGGACTTGAGGATAATCAAGTGGCAGTATGAAAGCTGGAA
 CTATTATCGTTATGATTTGGTATTTGATGATGATCCTGAAATCATAACATTGAAAGAAGAGAATTGATGC
 TGCTGTTAATTCTGGAGAACTGTGGTTGTAATTACTCCCAGGCTGTTACACTGCCATGATTAGCTCC
 CACATGGAGAGACTTGTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTTAATCTGGTGTGATGAGAAT
 GCCTTGCGGAATGAAAGGAGTCAACAGCTATCCAGTCTCTCATTTCGGTCTGGAATGGCCCCAGTGAATA
 TCATGGAGACAGATCAAAGGAGAGTTAGTGAGTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTG
 GACAGGAAATTGTCAACTCCATACAAACTGCTTTGCTGCTGGTATTGGCTGGTGTACACTTTGTTCAAA
 AGGAGGAGATTGTTGACTCACAGACAGCTCAGGCTTAGTGGCATGTTCTCAACTATTGGATGCTAA
 AGAAAATATTTGGAAGTAATAACATAATCTTCAGATTGAACTACTTCGGCAACACACTAGAGGATGTT
 GGCTCATCATCGGTGGCTTATTTTCAATTGGAAAAATGAAATGATCTGAGCTGAAAGAAACT
 AAAAATCTACTAAATGATCATATTCAAGTTGCAGGTTGACTGTTCTCTGCAACAGACATCTGAGTAA
 TCTGTATGTTTCAGCCCTCTAGCAGTATTTAAAGGACAAGGAACAAAGAATGAAATTCTCATGGAAA
 GAAGATTCTATGATACTTCAGCTTGCAAAAGAAAGTGTGAATTCTCATGTTACACGCTTGGACCTCAAA
 TTTCTGCCAATGACAAAAGAACATGGCTGTTGATTTCTGCCCCCTGGTGTGCCCCCTGAGCTTACT
 ACCAGAGTTACGAAGAGCATCAAATCTCTTATGGTCAGCTTAAGTTGGTACACTAGATTGACAGTTCATGA
 GGGACTCTGTAACATGTAACATTCAACACAGTGGTATTCACCAACAGTCAACAGTCAACATTGAGTA
 TGAAGGACATCACTCTGTAACCAAATCTGGAGTCATAGAGGATCTTGAATCCTCATGTTCTCCCTAC
 ACCCACCACCTTCAACGAAGTACACAAAGAAAACAAGCAAGTCTGGATGGTGTGATTCTATTCTCCGTG
 GTGTCATCCTGCCAAGTCTTAATGCCAGAATGGAAAAGAATGCCGGACATTAACACTGACTGATCAACGTGG
 CAGTATAGATTGCCAACAGTATCATTCTTTGTGCCAGGAAACGTTAAAGATAACCTGAGATAAGATT
 TCCCCAAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTGAATAGGGATGCTTATTCCCTGAGAAT
 CTGGGTCTAGGATTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTCAGTGAAGGATTTCTACAAGG
 GAAAATCATTGGTGTGATTGTTCTATGCTCTTGGTGTGGACCTTGCAGAATTGCTCCAGAATTGAGCT
 CTGGCTAGGATGATTAAGGAAAAGTGAAGGCTGAAAAGTAGACTGTCAGGTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTATCAAACGTGTAAGTTTATTCTACAGAAAGAGCAAAGAGAAAATTCAAGAAGAGCA
 GATAAATACCAAGAGATGCAAAAGCAATCGCTGCCATAATAAGTGAAGGAACTCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAAAAGTTCACTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTATGATGGGAATGAATGAACATTCTTAGACTGTCAGTTGACTGCCA
 GAATTATCTACAGCACTGCTAAAAGAAGGGTCTGCAAACCTTCTGTAAGGCGGTTATAAAATATT
 GACTTTGAGCTATAATATGGTTCACACATGAGAAAGAATAGGTCTCATGTTCTTGTATTGCT
 TTAAACAACCTTAAAAAATTAACAGCTTCTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTG
 GACCATAGATTGCTCCCCCTCGACGGACTTATAATGTTCTGAGGCTGGCTGCTGTTGAACATGAGTCTG
 ATCTACATAATGTCAGTTGATTAAGTCCACTTCCCTCACGTTTTGGCTGACCTGAAAGAGGTAAC
 TAGTTTTGGTCACTTGTCTTAAAGGCTTACCTGCTGTTGAGGAGATTCTCATGTTCTTCTTCTCA
 GATGTGGCACAGTAAACAAACCTGTTATGCTGTTATTATGAGGAGATTCTCATGTTCTTCTTCTCA
 AAGGTTGAAAAATGCTTTAATTTCACAGCCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC
 AAATTGAGCAACAGTAACTGCAACAAATTCTGAGTTGCTGATCATCCAGGAAACCTGAGGGAAAAATT
 TAGCAATTAACTGGGCAATTGAGGTTACCTAAATATGTTATCAAGTATTAGGTTCTATATTAAAGATATA
 TGTGTTCATGTTCTGAAATTGCTTCAAGAAAATTCTCCACTGATAGTTGATTTGAGGCACTAAATAT
 TTACATATTGCTCTGAACTTTGTTGACCTGTTACCTTACATTGGGTTTCTTCTATAGTTGG
 TTTTCACTCCTGTCAGTCTATTATATTCAAATAGGAAAATTACTTACAGGTTGTTACTGAGCTTAT
 AATGATACTGAGTTATTCCAGTTACTAGTTACTGTCAGAGGGCTGCCCTTCAGATAAAATTGACATAATA
 ACTGAAGTTATTGTTATAAGAAAATCAAGTATATAATCTAGGAAAGGGATCTCTAGTTCTGTTGTTAGA
 CTCAAAGAATCACAAATTGTCAGTAACATGAGTTGTTAGTTATAATTCAAGTGTACAGAATGGTAAAATT
 CCAATCAGTCAAAAGAGGTCATGAATAAAAGGCTGCAACTTTCAAAAAAAAAAAAAA

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FIGURE 426

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLHPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGIYDIDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTRWRDFAKEVDGLRIGAVNCGDDDRMLCRMKGVNSYPSLFIRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTFAAGGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDRDLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFKVGQGTKEYEIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPCRALLRPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSNIHEYEGHSAEQILEFIEEDLMNPSVVSLTPTFNELVTQRKHNEVWMVDFYSPWCPCQVLMPEWKRMARTLTGLINVGSGIDCQQYHSFCAQENVQRYPEIRFFFPKSKNAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLTPQTTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVKAGKVDCQAYAQTCQKAGKIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 427

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCGGACCCTGACTCTGCAGCCGAACCGGCA
CGGTTCTGTGGGACCCAGGCTTGCAAAGTGACGGTCATTTCTCTTCTTCTCCCTTGA
GTCCTTCTGAGATGATGGCTCTGGCGCAGCGGAGCTACCCGGTCTTGCGATGGTAG
CGGCGCTCTCGGCCGCCACCCCTGCTGGGAGTGAGGCCACCTGAACTCGGTTCTCAATT
CCAACGCTATCAAGAACCTGCCCCACCGCTGGCGCTGCCGGCACCCAGGCTCTGCAG
TCAGCGCCGCCGGGAATCCTGTACCCGGCGGGAAATAAGTACCAAGACCATTGACAACCTACC
AGCCGTACCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC
GCGGAGGGACGCAGCGTCAAATCTGTCGCTGCAGGAAGCGCCAAAAGCTGCATGC
GTCACGCTATGTGCTGCCCGGGATTACTGAAAAATGGAATATGTGTCTGATCAAA
ATCATTCCGAGGAGAAATTGAGGAACCATCACTGAAAGCTTGGTAATGATCATAGCACCT
TGGATGGGTATTCCAGAAGAACCCACCTGTCTCAAAATGTATCACACCAAAGGACAAGAAG
GTTCTGTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT
CCAAGATCTGTAACCTGCTGAAAGAAGGTCAAAGTGTGTACCAAGCATTAGGAGAAAAGGCT
CTCATGGACTAGAAATATTCCAGCGTTACTGTGGAGAAGGTCTGCTTGCAGGATAACAGA
AAGATCACCACATCAAGCCAGTAATTCTCTAGGCTTCACACTGTCAGAGACACTTAAACCAGCT
ATCCAAATGCAGTGAACCTCTTATATAAGATGCTATGAAAACCTTTATGACCTTCATC
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTCACTGTTAAGCATTCCAATAACACCTTCCA
AAAACCTGGAGTGTAAAGAGCTTCTTATGGAACCTCCCTGTGATTGCAGTAAATTACT
GTATTGTAATTCTCAGTGTGGCACTTACCTGTAATGCAATGAAACTTTAATTATTTTCT
AAAGGTGCTGCACTGCCTATTTCTTGTATGAAATTGGTACACATTGATTGTTAT
CTTGACTGACAAATATTCTATATTGAACATGAAGTAAATCATTGAGCTTATAGTTCTAAAG
CATAACCCCTTACCCATTAAATTCTAGAGTCTAGAACGCAAGGATCTTGAATGACAAAT
GATAGGTACCTAAATGTAACATGAAAATAGCTTATTTCTGAAATGACTATCTTAATG
CTTAAATTATATTCCCTTACGGCTGTGATAGTTGAAATAAAATTAAACATTAAAAAA
AAAAAA

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FIGURE 428

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA
PGILYPGGNKYQTIDNYQPYPKAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRHAM
CCPGNYCKNGICVSSDQNHFREGEIETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCCEGLSCRIQKDHH
QASNSSLRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 429

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGCTCCGGAGCCCAGCCC
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCTGTCACGGACCC
CAGCGTTACCATGCATCCTGCCGTCTCCTATCCTAACCGACCTCAGATGCTCCCTTGCT
CCTGGTAACTGGGTTTTACTCCTGTAACAACGTAAAGTCTGCTACAGAGAATAT
AGATGAAATTAAACAATGCTGATGTTGCTTAGTAAATTATGCTGACTGGTGTGCTTT
CAGTCAGATGTTGCATCCAATTTGAGGAAGCTCCGATGTCATTAAGGAAGAATTCCAAA
TGAAAATCAAGTAGTGTGCTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA
CAGGATAAGCAAATACCCAACCCCTCAAATTGTTGTAATGGGATGATGAGAGAGAATA
CAGGGGTCAAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCCAT
TCAAGAAATTGGGACTTAGCAGAAATCACCACTCTGATCGCAGCAAAAGAAATATCATTGG
ATATTGAGCAAAGGACTCGGACAACATAGAGTTTGAAACGAGTAGCGAATATTGCA
TGATGACTGTGCCTTCTTCCTGCATTGGGATGTTCAAAACCGAAAGATATAGGGCGA
CAACATAATCTACAAACCACCAAGGGCATTCTGCTCCGGATATGGTGTACTGGAGCTATGAC
AAATTGAGTAGTGACTTACAATTGGATTCAAGATAATGTGTTCTCTGTCCGAGAAATAAC
ATTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTCTCATACTCTTCACATGAA
AGAAGATAACAGAAAGTTAGAAATATTCCAGAATGAAGTAGCTCGCAATTAATAAGTAAAA
AGGTACAATAAACTTTTACATGCCGATTGTGACAAATTAGACATCCTCTGCACATACA
GAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTAGGCATATGTATGTGTTGG
AGACTTCAAAGATGTATTAACTCCTGGAAACTCAAGCAATTGCTATTGACTTACATTCTGG
AAAACGACAGAGAATTCCATCATGGACCTGACCCAACTGATACAGCCCCAGGAGAGCAAGC
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTCCAGAAACTAGCACCAGTGAATATAG
GTATACTCTATTGAGGGATCGAGATGAGCTTAAAACTGAAAAACAGTTGTAAGCCTTC
AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTCATAATTCTATGTGTAT
TTTATTTGAATAAACAGAAAGAAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 430

MHPAVFLSLPDLRCSLLLLTVWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRCFSQM
LHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYSKPTLKLFRNGMMMKREYRGQ
RSVKALADYIRQQKSQDPIQEIRDIAEITTLDRSKRNIIIGYFEQKDSNDNYRVFERVANILHDDC
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN
GEELTEEGLPFLIFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP
ADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPDTAPGEQAQDV
ASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:**Signal peptide:**

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 431

GAGCAGGACGGAGCC**ATGG**ACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGCA
GGCTGGCTGCTGCTGCTGCTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGCGTG
GACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCACGACAATTCTCGCTGGCAGTG
CGGGGTTGCGGTTGGGACTCCCCGCAAGAATGACCGCGGCCCTGGATCTCACGGGCTTCTG
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTAACCTCACCTCG
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTGCTACAGC
TGTGTGGGCTTGAGCCGGAGGCCTGCCAGGGTACATGCCGCCGTCGTGAGCTGCTACAAC
GCCAGCGATCATGTCTACAAGGGCTGTTGACGGCAACGTCACCTGACGGCAGCTAATGTG
ACTGTGTCTTGCCCTGTCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGATGGAGTAACA
GGCCCAGGGTTACGCTCAGTGGCTCTGTGCCAGGGTCCCGCTGTAACTCTGACCTCCGC
AACAAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCTCCAGAGCCCACG
ACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC
ACCAAACCCATGCCAGGCCAACAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCCTCC
CGGGATGAGGAGGCCAGGTTGACTGGAGGCCTGCCACCAGGACCGCAGCAATTCAAGGG
CAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCT
GGATTGGCAGCCCTCTGTTGGCCGTGGCTGCTGGTCTACTG**TGA**GCTTCTCCACCTGGA
AATTTCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTTCTCATCACCTCCTGTTCCA
CCACTGGACTGGCTGCCAGCCCCCTGTTTCAACATTCCCCAGTATCCCCAGCCTCTGC
TGCCTGGTTGCGGCTTGGAAATAAAACCGTTGTATATATTCTGCCAGGGTGTCTA
GCTTTTGAGGACAGCTCCTGTATCCTCTCATCCTGTCTCCGCTTGTCTTGTGATG
TTAGGACAGAGTGAGAGAAGTCAGCTCACGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC
TACTCACTTCTCCTAGCCAGCCTGGACTTGGAGCGTGGGTGGGACAATGGCTCCCC
ACTCTAAGCACTGCCTCCCTACTCCCCGATCTTGGGAAATCGGTTCCCCATATGTCTTCC
TTACTAGACTGTGAGCTCCTCGAGGGGGGCCGGTACCCAATTGCCCTATAGTGAGTCGTA

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FIGURE 432

MDPARKAGAQAMIWTAGWLLLLLRGGAQALECYSCVQKADDGCSPKMKTVKCAPGVDVCTE
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAIFIQLQQCAQDRCNAKLNLTSA
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVSCYNASDHVYKGCFDGNVTLTAANVT
VSLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPE
PTTVASTTSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGVEHEASRDEEPRLTGGAA
GHQDRSNSGQYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 433

CGGGACTCGGCGGGCCTCCTGGGAGTCTCGGAGGGACCGGCTGTGCAGACGCCATGGGAGTT
GGTGCCTGGTCTTCCTCTGCAGCCTGCTGGCCCCATGGCCTGCCAGTGCAGCTGAAAAGGA
GAAGGAAATGGACCCTTTCATTATGATTACCAGACCCCTGAGGATTGGGGACTGGTGGTGC
TGTGGCCTCTCTCGGTTGGATCCTCTTATCCTAAGTCGCAAGTGCAAGTGCAGTTCAA
TCAGAACGCCCCGGGCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCCAATGC
AACAGAGCCCCAGAACGAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG
GCGGCTGCTTAACCTTGGATGCAAATGTCGATGCTTAAGAAAACCGGCCACTTCAGCAACA
GCCCTTCCCCAGGAGAACGCAAGAACCTGTGTGTCCCCCACCCATCCCCCTAACACCATT
CCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCCCTGCCACCTC
CCGTGATGTGTGTGTGTGTGACTGTGTGTTGCTAAGTGTGGTCTTGTGG
CTACTTGTGGATGGATTGTGTTGTTAGTGAAGTGTGGACTCGCTTCCCAGGCAGGG
GCTGAGCCACATGCCATCTGCTCCTCCCTGCCCGTGGCCCTCCATCACCTCTGCTCCTA
GGAGGCTGCTTGTGCCCGAGACCAGCCCCCTCCCTGATTAGGGATGCGTAGGGTAAGAGC
ACGGGCAGTGGTCTTCAGTCGTTGGGACCTGGGAAGGTTGAGCACTTGTCACTCATTCT
TCATGGACTCCTTCACTCCTTAACAAAACCTGCTTCCTTATCCCACCTGATCCAGTCT
GAAGGTCTTAGCAACTGGAGATAAAAGCAAGGAGCTGGTGAAGCCCAGCGTTGACGTCA
CAGGCTATGCCCTCCGTTAATTCTCCAGGGCTTCCACGAGGAGTCCCCATCTGCC
CCGCCCTTCACAGAGGCCCGGGATTCCAGGCCAGGGCTTCACTCTGCCCTGGGAAT
GTGTCCCCTGCATATCTCTCAGCAATAACTCCATGGGCTCTGGGACCTACCCCTTCAACC
TTCCCTGCTTGTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC
AATTGGGTCTCTGGCAGGAATAGTTGAAGGACTCTGTTCCGTTGGGCCAGCACACCGGGA
TGGATGGAGGGAGAGCAGAGGCCTTGCTTCTGCCTACGTCCCCCTAGATGGCAGCAGAG
GCAACTCCGCATCCTTGCTCTGCCCTGCGTGGTCAAGAGCGGTGAGCGAGGTGGGTTGGAG
ACTCAGCAGGCTCCGTGCAGCCCTGGGAACAGTGAAGAGGTTGAAGGTATAACGAGAGTGGG
AACTCAACCCAGATCCGCCCTCCTGCTCTGTGTTCCCGCGGAAACCAACCAACCGTGC
GCTGTGACCCATTGCTGTTCTGTATCGTATCTACCTCAACAAACAACAGAAAAAGGAAT
AAAATATCCTTGTTCCT

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FIGURE 434

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHHDYQTLRIGGLVFAVVLFSVGILLILSRRCKC
SFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRRLEPLDANVDA

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FIGURE 435

GGTCCTTAATGGCAGCAGCCGCCGTACCAAGATCCTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCC GGCTGGCGAGCCGACCCTCACTCTCTTGCTATGACATCACCGTCA
TCCCTAAGTTAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAAGAAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTGGCAGTCAGTTCGATG
GGCAGATCTCCTCCTCTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCATGTCCTTCATTACTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTGCCATGTCCTCAGGCACAACCCAACTCAGGCCACAGCCACCCACCC
TCATCCTTGTGCTGCCTCTCATCATCCTCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTGATTCTTTGCCAACAAATTAA
CCAGCAGTTACCTAACATATTATGCAATTCTCTGGTGCTACCTGATGGAATTCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTCTCTCTTTGGAAAGAAAA
TCAAGTACTCTTGAAATGATGATCTCTTGCAAATGATATTGTCAGTAAATAATCACG
TTAGACTTCAGACCTCTGGGATTCTTCCGTGTCTGAAAGAGAATTAAATTATTAAT
AAGAAAAAATTATATTAAATGATTGTTCTTAGTAATTATTGTTCTGTACTGATATTAA
ATAAAGAGTTCTATTCCAAAAAAAAAAAAAA

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FIGURE 436

MAAAAATKILLCLPLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWC
AVQGQVDEKTFLYDCGNKTVPVSPLGKKLNVTAWKAQN
PVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKM
KEKWENDKVVAMSFHYSMD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATT
LILCCLIIILPCFILPGI

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FIGURE 437

GTTCTCCTTCCAGGCCAAATCCCAGGCATGGTGAATTATGAACGTGCCACACCATGAAGCTTTGTCAGG
TAACTGTGCACCAACACACCTGGAATGCATCCTGCTCCGTTCGTCTACCTCACGGCGCAAGTGTGGATTCTGT
GTGCAGCCATCGCTGCTGCCGCCAGCCGGGCCCCAGAACTGCCCTCCGTTGCTCGCAGTAACCAGTTCA
GCAAGGTGGTGTGCACGCGCCGGGCCCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC
TCATGGAGAACAAACATCCAGATGATCCAGGCCACACCTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG
GCAGGAACACTCCATCCGGCAGATTGAGGTGGGGCCTCAACGGCTGGCCAGGCTAACACCCCTGGAGCTGTTCG
ACAACGGCTGACAGTCATCCCTAGCGGGCCTTGAAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGAACA
ACCCCATCGAAAGCATCCCCCTTACGCCCTCAACCGGGTGCCCTCCCTATGCCCTGGACTTGGGGAGCTCA
AGAAGCTGGAGTATCTCTGAGGGAGCTTTGAGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCATGTGCA
ACATTAAGACATGCCAATCTCACCCCCCTGGCTGGAGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTCCCTG
AGATCAGGCCTGGCTCCATGCCCTGAGCTCCCTCAAGAAGCTGGGTATGAACTCACAGGTCAAGCCTGA
TTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGGAACCTAACCTGGCCACAATAACCTCTCTTGC
CCCATGACCTCTTACCCCGTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCTTGAACCTGTGATTGTG
ACATTCTGTGGCTAGCCTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTC
CCATGCACATGCCAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCAGTGCTCTGCCCTTCATCATGG
ACGCACCTCGAGACCTCAACATTCTGAGGGCTGGATGGCAGAACCTAACGACTCTGTGCGACTCCCCCTATGCTCCG
TGAAGTGGTGCTGCCAATGGACAGTGCTCAGGCCACGCCCTCCGCCACCAAGGATCTGTGCTCAACGACG
GCACCTTGAACCTTCCACGTGCTGCTTCAAGACACTGGGTGACACATGCACTGGTACCAATGTTGCAGGCA
ACTCCAAAGCCTCGGCCCTACCTCAATGTGAGCAGGGCTGAGCTAACACCTCCAACGACTTCTTCAACCACAG
TAACAGTGGAGACCACGGAGATCTGCCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTACCACGTCCACTG
GTTACAGCCGGCATATACCACCTCTACCAACGGTGTCACTCAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC
CCGGACAGACACCACTGACAAGATGCAGACAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT
GCTTGTGGCAGTGACTIONGTGCTGCCCATGTTGATTGTCTTCTATAAAACTTCGTAAGCGGCACAGCAGC
GGAGTACAGTCACAGCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGAG
CAGCAACAGCAGCTCCGTCCGGTGTACAGGTGAGGGGGCAGTAGTGCTGCCACAATTGACCATATTAAC
ACAACACCTACAAACCAAGCAGCACATGGGGCCACTGGACAGAAAAGCAGCCTGGGAACCTCTGCACCCCACAGTCA
CCACTATCTCTGAACCTTATATAATTCAAGACCCATACCAAGGACAAGGTACAGGAAACTCAAATATGACTCCCCT
CCCCCAAAACTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTT
TTCTTGATATGCTTATATAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAAAATTAAAGACAAAA
AGTCAAAACA

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FIGURE 438

MKLLWQVTVHHHTWNAILPFVYLTAQWILCAAIAAAASAGPQNCPSCSNSQFSKVVCTR
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVQLGRNSIRQIEVGAFNGLASLN
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE
GAFEGLFNLKYLNLMCNIKDMPNLTPLVGLEELEMMSGNHFPEIRPGSFHGLSSLKKLWVMNS
QVSLIERNADFGLASLVELNLAHNNLSSLPHDLFTPLRYLVELLHHNPWCDCDILWLAWWL
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVTYTCMVNVAGNSNASAYLNV
STAELNTSNYSFFTHTVETTEISPEDTRKYKPVPTTSTGYQPAYTTSTVLIQTTTRVPKQV
AVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE
IIQVDEDIPAATSAAATAAPSGVSGEAVVLPTIHDHINYNTYKPAHGAHTENS LGNSLHPT
VTTISEPYIIQTHTKDKVQETQI

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FIGURE 439

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG
TCAGTGTGTCCTGATGGTCTCGCTGCCCTTGCTGCTACCAGGCCATGCTCTTGTCTGC
CCAGCTGTTGCTCTGAGATCACAGTCTTATTCTTAAGTGACGCTGCGGTAAACCTCAA
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
GATCAGATATCTTTAAGAACGACTCTCATGAAAAAGTCCTGGTGGAAATAGTGAAAAAAT
GTGGTGTGTGACATGTAAGGTTAACACGTTGCTTAATAAATCACTGCCCTGATC
TTCACTAAAATTGTAAGGTTAACACGTTGCTTAATAAATCACTGCCCTGC

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FIGURE 440

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQVAKLNPPPEALAAKLEVK
HCTDQISFKKRLSLKKSWWK

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FIGURE 441

GAACATTTAGTCCAAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG
GGGTTGCTGGTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC
ACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCATGGCAGGCTCCAG
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAACGCCACCAGCAA
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCGGAAAGATGGAGGTCAAGCAGAACGGGC
AGAGGATGAACGTGGAAAGTCCGGTTCAACGCCCTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAAGCAGCACAGCCAGGCCCTGGGAAGTTCTTCAGGACATCCTCTGGGAAGAGGC
CAAAGAGGCCAGCCGACAAGTGATCGCCCACAAGCCTACTCACCTCTCTAAGTTAGA
AGCGCTCATCTGGCTTTCGCTTGCAACTCCCACGACTGTTGTACAAGCTCAGG
AGGCGAATAATGTTCAAAGTGA

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FIGURE 442

MPSPGTVCSSLGGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG
QAEGAEDELEVRFNAPFDVGIGKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 443

CGGCCACAGCTGGCATGCTCTGCCTGATGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG
TGAACCCCAGGGTGCTCCGCACGGACCCCAGATGTCAAGAATTGAACACGTGGCTGCTGTTCT
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCCTGATAGTCGTGATCGGGATGCTCGTGCCT
CTGCTGGACTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT
ATGTCCCCCACCTAAGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATCTTACA
CCTCTACTTGAGTATGTCCTAACCCCTGAGCCCCCACGCCTGGGCCAGAGTCTTGTCCCC
CGTGTGCGATGTGTTAGGGTCAGCCTCTCCAGAAAGTGAGATCATGGACAAAAGGGCAA
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACACGCCG
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTAAATGTTAGAGACAATGGA
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC
AAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCAACCCTAACAAACAACTGAAG
CGAGAGCTGTGGCTTGCTTGGCTCACAGTGGGCACAGCGGTAGGGCGTCAGTCATGTTGCT
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAAACCTCC
CTGCTCCTGGCACCAGCCGTTTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCATTCTG
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTCTGTGGACACGGGCAGCAGAGTG
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTGGCCAACCCCTGGTCAGGGCA
GAGGGAGTTGGGTGGTCAGGCTCTGGCTCACCTCCATCTCCAGAGCATCCCCCTGCTGCAG
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGAGCCTCCTGTTCATAAC
ACAGGTTACCCCTACAAACCACTGTCCCCACACAACCCCTGGGATGTTAAAACACACACCTC
TAACGCATATCTTACAGTCAGTCACTGTTGTCTGCCTGAGGGTTGAATTTTTAATGAAAGTGC
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 444

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLGLVHLGQLLIFHIYLSMSPTLSPRSPQGWV
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKGKSQEEIKSMRTQQAQ
QEAEELTPRPAGVVPGA

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FIGURE 445

AGGCGGGCAGCAGCTGCAGGCTGACCTGCAGCTGGCGGAATGGACTGGCCTCACAAACCTGC
TGTTTCTTCTTACCATTCCATCTTCCTGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA
GGAAGGGGCAAGGGCGGCCTGGGCCCTGGCCCTGGCCCTACCCAGGTGCCACTGGACCTGG
TGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTGCAGCTGTGGA
TGTCCAACAAGAGGAGGCCTGTCTCCCTGGGCTACAGCATCAACCACGACCCAGCCGTATCC
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGAACCCCTCACCATGCAGG
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCCTGCC
CGCCACCGCCCCGCACAGGGCCTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT
GCACCTGCATCTCTGAATCACCTGGCCCAGAACGCCAGCAGCCGAGACCATCCTCCT
TGCACCTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTGAAAGCAAG

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FIGURE 446

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRGPLAPGPHQVPLDLVSRMKPYARMEYE
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGC
VNPFTMQEDRSMVSVPVFSQVPVRRRLC PPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 447

GGAGTGCAGATGGCATCCTCGTTCTCCAGACAAGCTGCAAGACGCTGACC**ATGCCAAGA**
TGGAGCTCTCGAAGGCCTCTCTGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT
CACTCAGCTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGTGGCACACAGAAGGTGC
CCAAGCCCCGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTGGATG
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACACTGGGAGACTGGGATGACCGGT
TCTCCTCCGGAGCTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAGAACAG
GGGAGAGGTGCCAAGTTCAATTGAACCTACACCAGCCAAGAGAGGTGAGAAAGGACTAC
TGGAATTGCCACGTTGCAAGGCCATGTCACCCCACCTCTCCGATTTGGAGGGAAGCGGTTGA
TGGAGAAGGCTCCCTCCCTCCCTGGGGCTTGTGGCAAAAATCCTATGTTATCC
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTCCTCCTGCTACTAACAGAC
TTGCTACTCACTGGAACCCCTGCCTGTGGCTCAAACATGAGCCTTGCTGCTGTTCCCT
GTCCTGTCAGGTCTCTGGGATGGTGGCCACATGATGTATTACAAGTCTCCAAGCGACT
GTCAACTGGTCCAGAAGACTGGAGACCACATGTTGAAATTATGGCTGGCCTTCTACATG
GCCTGGCTCTCCTCACCTGCTGCATGGCGCTGTCACCACCTCAACACGTACACCAGG
ATGGTCTGGAGTTCAAGTGAAG**CATAG**TAAAGAGCTCAAGGAAAACCGAACTGCCAACCA
CATCACCATCAGTGTTCCTCGCGGCTGTCAGTGCAGCCCCACCGTGGTCCTTGACC
AGCTACCACCAAGTATCATAATCAGCCCACACTCTGTCTCTGAGGGAGTCGACTTCACTCC
GAGCTGCGGAACAAGGGATTCAAAGAGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA
TCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTGGGAGTAGGCTTGAGCCCTACCT
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGCTCTGAGCATGGTTTTA
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTAAGCTTAAGGGATTCTGGGTGCCA
CTGCTCTCTTCTACAGCTCCATCTGTTCACCCACCCACATCTCACACATCCAGAA
TTCCCTTCTTACTGATAGTTCTGTGCCAGGTTCTGGCTAAACCATGGAGATAAAAGAAG
AGTAAAATACACTCCCGACCTAAGGATCTGAAA

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FIGURE 448

MAKMELSKAFSGQRTLLSAILSMLSLSFSTSLLSNYWFVGTQKVPKPLCEKGIAAKCFDMPV
SLDGDTNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCETVEEPGERCRSFIELTPPAKRGE
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQQLPPA
TNRLATHWEPCPCLWAQTERLCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLELWLG
LLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 449

CCCCACGCGTCCGCCAACGCGTCCGCCAACCGGTCCGCCAACCGGTCCGCCAACCGGTCCGCCAACCGGTCCGCC
ACGGGTCCGGTGCAAGCTCGCGCCGCACACTCGCTGGTGGAGGGAAAGGAGGCCGGCCTCTCGCGCTCCCCG
CGCCCGCTCCGCACCTCCCCAACCGGCCGCCGCCGCCGCCGCCAACAGCATGAGTGAGCCGCTCTCT
GCAGCTGCCGGGGCGGAATGGCAGGGCTGTTCCGGAGTAAGGTTGGAGTTTTCCCCCACAAACGT
GACGGACATTAAACCAGACTGTCAGATCTGGGGAGTCGGAGGCCAGGGAGCTCGAGGCCAGCTGGTAGTTGGGAAACT
CACAGTCCGAACCTGCAGAGGGAAAGGAGGCCAGGGAGCTCGAGGCCAGCTGGAGCTGGAGCTGGTAGTTGGGAAACT
TGCGGGTCTTAGAAGTGCCTCCCCGGCTCTGGCGGGGGCTTGAGCGCCGGAGCCGAGCAGCAAAGTGGAGACAT
TGTGCGCTGCCAGATCCGCCGGCCGCCGGCTGCCCTCGGAAACACAGAGGGTCTCTCTGCCCTGCA
TATAATTAGCCTGCACACAAAGGGAGCAGCTGAATGGAGGTGTCACTCTCTGGAAAAGGATTTCTGACCGAGCG
CTTCATAATGGACATTCTCCAGTCCTCTGGAAAGATCTCGCTATGGATTCTCGCTCTGTCCTGTCAT
ACTGGCTGTGAGGGGCCCTCGGGGGTGGTCTGCTGCTTTCAGATGCTGCCCGCCGCC
CCAGGGGTGCCCCAGCTGTGAGGGGCCCTGCTGCTTTCAGATGCTGCCCGCCGCC
CCCACAACCTGTCGGGCTGCTGGGCTTGTCCCTGGCTACAACAGCTCTCGGAGCTGCCGCCAGGCG
CGGGGTTAATGCACTGAGCTACGGCTATCTGGATCACATCACATCTGTCCTGGTGCAGGGGAGCCCTTCA
AACTGCGCCGAGTTAAGGAACCTACGCTGAGTTCACAGGATCACCAACTGCCAACACCACCTCCGGCCA
TGCCCAACCTGCGCAGCGTGGACCTCTGTCACACAAGCTGCAGCGCTCGGCCGACCTCTCACGGGCTGC
GGAAGCTCACACAGCTGCAATATGCGGGCAACGCCATCCAGTTGTGCCCTGCGCATCTCCAGGACTGCCGCA
GCCTCAAGTTCCTGACATCGGATACAATCAGCTCAAGAGTCTGCCGCCAACCTTCCGCCGCTCATCTCCCTGC
TCACCGAGCTGCACTCGAGCACACGGACTTGGTCAAGGTGAACACTTCGCCAACCTCCGCCCTCATCTCCCTGC
ACTCGCTCTGCTGCCGGAGGAACAAGGTGAGGATTGTGTCAGCTGCTGGACTGGTTTGGAACCTGGAGAAAA
TGGACTTGTGGCAACGAGATCGAGTACATGGAGCCCCATGTGTCAGGACCGTGCACCTGCAGTCCCTGC
AGCTGGACTCCAACCGCCTCACCTACATCGAGCCCCGGATCTCACACTTGGAAAGTCCCTGACAAGCATCACCC
TGGCGGGAAACTGTGGGATTGCGGGCAACGGCTGTGCCCCCTAGGCTGTGGCTCAGCAACTTCCAGGGCGCT
ACGATGGCAACTTGCACTGAGCTGCCAGGGGAGTACGCACAGGGGAGGAGCTGGACGCCGTGACGCCCTTCC
ACCTGTGCAAGGATGGGGCGAGGCCACCAGCGGCCACCTGCTCTGGCCGTACCAACCGCAGTGATCTGGGGC
CCCCCTGCCAGCTGCCACCACGCTCGGGACGGCGGGAGGGGAGGGCAGCACGCCACATTGAGCCCTGCCACCG
TGGCTCTTCAAGGGCGAGCGACGGCGAGAATGGCTGAGTACCTGGGCTCTGGCTGAGTCCAGGGCACATGGCCCTCA
TCTTCTCTTCTCATCGTGTCTGGTCTACGTTGCTCTGGAAAGTGTGCTTCTGGCCAGGCTCAGGAGCTCA
GACAGTGTGTTGTCAGCAGCGAGGAAGCAAAGAGAACAGACCATGCACTAGATGGCTGCCATGTGCTGCC
AGGAATAACTACGTTGATTACAAACCGAACCATGGAGGGGCTGTGATCATCAAGAGTATGGCTGTGTA
CCTGCCAACAGCAGGGGGAGGGAAATGGAGGTCTGATTGTCCTGCTCTCAACCCATGCGTACCAAATA
CGCTGGGCAAGGGGGAGGGGGAGGGGGAGGGGGAGGGGGAGGGGGAGGGGGAGGGGGAGGGGGAGGGGG
TGAAACTTTAAGGGGATCTCTCCAGAGAGACTTGACATTAGTTAGTGTCTTAAATTCATGAGAACCTTCCCTCCC
AACACAACAAAAACCCCCACACCAACCTTCAGGACAGTCTATCTAAATTCATGAGAACCTTCCCTCCC
TTTGAAGATCTGTCATATTCAAGGAGTCTGAGACTGAGAGTCAAAAGGGCATATGAGAACAGAGAGAATAATCGT
CTTGTGTTTATGCTACTCTCCCAACCTGCTCATGATTAACACATGCTATGAGAACATCTTAAAGTCCATACGC
ATTTCATGAAGAACATTGGAAAGAGGAATCTGCAACTGGGAGCTTAAGAGCAAATGATGACCATAGAACGCTA
TGTTCTTACTTGTGTGTGTGTTCTGCTGTTCTGCTGCTCTGGTAGGCAAGAACAGTGTCTACACA
AACGGGAATTTAGTCACATCATTTCTGCTGCTGCTGAGCTCTGGAGATTGGTGGGGGGAGGTGGGGGG
AACGGCAGGAATAAGGGGAAAGTGGTAGTTAACTAAGGTTTGTAAACACTTGAATCTTCTTCTCAAATT
ATTATCTTAAGCTCAAGAAACATTGCTCTGACCCCTCTAACGAAACTACTAACGATTAAAAGAGAAATCTAATT
TTTAAAGGTGTAGCACCCTTTTTTATCTCTCCACAGGGGGCTAACATCTGCTGCTATCTGAA
GAACCTAACGGCAACATTCACTCGTCTGGCATGGTGTGATGGATTGACCCCTCATGGCAGTACCTTCCAG
CTGATTAAGGTTCACTGAGTGTGTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGG
GACACTCTCACACCAGTCTTAGCCCTAGTAGTTTGTGACAGCTTGTGCTGATTTGGGATTTGGG
CTCTGCTGCACTCAGAAAAAAATAGGCAGTCCCTGATGCTCAGATCTTGTGATTTGGG
TACCCAAATGCCCTATACTCCCAGAACACTAACAGTACCATCGAACAGGAAGGTTATTCCAGTAAAAGGAA
ATAGTTCTCAACATTAAATATCTCTGAACTCATCAAAGTAGAAGAGGCCAACCTTCTCTGC
CTTCAGAACGGCAGACATTGGTATGATTAGCATCAAACACATTATGAGTATATGTAAGTAATCAGAGGGG
CAAATGCCACTTGTATTCTCCCAAGTTTCCAAGCAAGTACACACAGATCTGCTGAGGATTAGGGGCCACTT
GTGTTCCGGCTTATTTAGTCAGACTGCTGAGCTAGTTGATGCTGCTAGTCTATGCACTGACATGCCAGTAGAACAG
GGCATTGATGGATCACATGAGATGGTAGAAGGAACATCATCACATACCCCTCTCACAGAGAAAATTATCAAAGAA
CCAGAAATTATATCTGTTGGAGCAAGAGTGTCAATGTTCAAGGTAGTCAAAATAACATAAAATTATCTCC
TCTAGATGAGTGGCAGTGTGGCTGATTGGGCTGCCATTGACAGAAATGTCATAAAGGAAATTAGCTAGAA
TATGACCATTAATATGTGCTCTGAAATATATTTGAGATAGGTTAGAATGTCA

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FIGURE 450

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLRCERLLYCEALNLTEAPHN
LSGLLGLSLRYNSLSELРАGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSNNQIT
QLPNTTFRPMPLRSVDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKF
LDIGYNQLKSLARNASFAGLFKLTELHLEHNDLVKVNAHFPRILISLHSLCLRRNKVAIVSSL
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQLDSLQDSNRLTYIEPRILNSWKS LTSITLAGNL
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDavyAFHLCEDGAEPTSGHLLSAV
TNRSDLGPPASSATTLADGGEQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII
NEYGSCTCHQQPARECEV

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FIGURE 451

TTGAGCCGAGGTGAGCTCCTGCGCGTCCGGGGCGTTCCAGTCACCCCTCCGCCGTAC
CCGGCGCGCCCCGAGGGAGTCTCCTCCAGACCCCTCCCGTTGCTCAAACATAATACGGA
CTGAACGGATCGCTGCAGGGTGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT
ACCATCCATAGCCAGATAGATTATCTTACACTGAACGTGATCAAGTACTTGAAAATGACTTCG
AAATTATCTGGTGCCTCATACTTACGTGACTGAGTCTTCAACCACCTTTCTCTCCAA
CTAGACCAGAAAAGGTTCTACTAGTTCTTGTGATGGATTCCGTTGGATTACTTATATAAA
GTTCCAACGCCCATTTCATTATATTATGAAATATGGTGTACGTGAAGCAAGTTACTAAT
GTTTTATTACAAAAACCTACCCCTAACATTATACCTTGGTAACGGCCTCTTGCAGAGAAAT
CATGGGATTGTTGCAAATGATATGTTGATCTTATTCGGAACAAATCTTCTCTGGATCAC
ATGAATATTTATGATTCAAGTTGGGAAGAAGCAGACACCAATATGGATCACAAACCAGAGG
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGAACAGATGTAaaaACATAAGCCTT
CCTACTCATTACATGCCTTACAATGAGTCAGTTCTTGAAGATAGAGTTGCCAAAATTGTT
GAATGGTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTTGTGATGAC
ATGGGCCACCATTGGGACCTGACAGTCGCTCATGGGCCGTGCTTCAAGATATTGACAAG
AAGTTAGGATATCTCATACAAATGCTGAAAAGGCAAAGTTGGAACACTCTGAACCTAATC
ATCACAAGTGTGATGGAAATGACGCACTGCTCTGAGGAAGGTTAATAGAACTTGACCAGTAC
CTGGATAAAGACCACTATACCCCTGATTGATCAATCTCCAGTAGCAGCCATCTGCCAAAAGAA
GGTAAATTGATGAAGTCTATGAAGCACTACGCTCATCCTAATCTTACTGTTACAAA
AAAGAAGACGTTCCAGAAAGGTGGCATTACAATACAACAGTCGAATTCAACCAATCATAGCA
GTGGCTGATGAAGGGTGGCACATTACAGAATAAGTCAGATGACTTCTGTAGGCAACCAC
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTAGGCCATGGTCTGCTTCAGA
AAGAATTCTCAAAAGAAGCCATGAACTCCACAGATTGTACCCACTACTATGCCACCTCCTC
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTAGCA
ATGCCAAGGGTGGCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTAAACCAGCA
GAATATGACCAAGAGGGTCATACCCATTTCATAGGGGTCTCTTGGCAGCATTAGTG
ATTGTATTTTGTAATTTCATTAAGCATTAACTCACAGTCACACTACACACACACACACA
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCTTAATGTTACTTGAAGTGGATTGCA
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTAAAGGTTCAAATTCTGGAAACCAAGTT
CCAAACATCTGCAGAAACCATTAAGCAGTTACATATTAGGTATACACACACACACACA
CACATACACACACACGGACAAAATACTACACCTGCAAAGGAATAAGATGTGAGAGTATGT
CTCCATTGTTACTGTAGCATAGGGATAGATAAGATCCTGCTTATTGGACTTGGCAGAT
AATGTATATATTAGCAACATTGCACTATGTAAGTACCTTATATTGCACTTTAAATTCT
CTCCTGATGGGTACTTTAATTGAAATGCACTTATGGACAGTTATGTCTTATAACTGATTG
AAAATGACAACCTTTGACCCATGTCACAGAATACTTGTACGCATTGTTCAAACACTGAAGGA
AATTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAAATTGAGAGAAGAAGAA
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTGAACCTTGAATTGGAGATGTATTCC
CAACAGCAGAATGCAACTGTGGCATTCTTGTCTTATTCTTCCAGAGAACGTGGTTTCA
TTTATTCTTCCCTCAAAAGAGAGTCAAATACTGACAGATCGTCTAAATATATTGTTCTGT
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTCTATTAATGAAGACAC
CATGAATATACTTTCTTCTATAGTCAGCAATGGCCTGAATAGAAGCAACCCAGGCACCAT
CTCAGCAATGTTCTTGTATTGCTCCTTGAAAATTAAACTATTACATTAAATT
ACATTAACAAATTGGATAAAAAAAAAAAAAAA

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FIGURE 452

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSDGFRWDYLYKVPTPHFHYIMKYGVHVQ
VTNVFITKTYPNHYTLTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIWIT
NQRAGHTSGAAMWPGBTDKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED
PDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL
DQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKNSRIQP
IIAVADEGWHILQNKSDDFLLGNHGDNALADMPIFLAHGPFRKNFSKEAMNSTDLYPLLC
HLLNITAMPNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYFIGVSLGS
IIVIVFFVIFIKHЛИHSQIPALQDMHAEIAQPLLQA

Important features:**Signal Peptide:**

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 453

GGCCGCCTGGAATTGTGGAGTTGTCTGCCACTCGGCTGCCGGAGGCCAAGGTCCGTGAC
TATGGCTCCCCAGAGCCTGCCTCATCTAGGATGGCTCCTCTGGCATGCTGCTTGGCTGCT
GATGGCCGCCTGCTCACCTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGACCAA
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA
TGCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTCAGCCAGGGCAGGC
TGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGAAAGAGAGGCAAAACTCCA
ATATGAGGACAAGTTCCGAAATAATTGAAAGGAAAAGGCTGGATATCAACACCAAACACCTA
CACATCTCAGGATCTCAAGAGTGCAGTGGCAAAATTCAAGGAGGGGCAGAGATGGAGAGTTC
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTTCCGCCATTGAGGAAGTGA
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT
CAACAAGTTCAATAGTTCCAGCTCCAGTTGAAAGAGAAGATTGCTGCGCTTTGATCTTGA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCCTTGTTGGTGGTCTTCAAGTGGT
GATCAATGGGCTGAACAGCACAGAGCCCTCGTAAGGAGTATGCTGCGTTGTGCTGGCGC
TGCCTTCCAGCAACCCCAAGGTCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT
GCTGGTCATCCTGGCACGGAGCAGCGCTCACTGCAAAGAAGAAGGTCTTGCACTGTG
CTCCCTGCTGCGCCACTTCCCTATGCCAGCGCAGTTCCTGAAGCTGGGGCTGCAGGT
CCTGAGGACCTGGTCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCTGGTCACACTG
CTACGACCTGGTCACGGAGAAGATGTTGCCAGGTACACCTCTGCCAGGCCTGTGGAACAGGGCTG
CCCAGAGAAGCTGCAGCAGTATGCCAGGTACACCTCTGCCAGGCCTGTGGAACAGGGCTG
GTGCGAGATCACGGCCACCTCCTGGCGCTGCCGAGCATGATGCCGTGAGAACAGGTCTGCA
GACACTGGCGTCCCTGACCACCTGCCGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG
GACACTGGCCAGCCTGCAGGCTGAGTACCAAGGTGCTGCCAGCCTGGAGCTGCAGGATGGTGA
GGACGAGGCTACTTCCAGGAGCTGCTGGCTCTGTCAACAGCTGCTGAAGGAGCTGAGA**TG**
AGGCCCCACACCAGGACTGGACTGGATGCCCTAGTGAGGCTGAGGGTGCCAGCGTGGGTG
GGCTCTCAGGCAGGAGGACATCTGGCAGTGCTGGCTGGCCATTAAATGGAAACCTGAAGG
CCAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 454

MAPQLPSSRMAPLGMILLGLLAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEELD
AEVLEVFPTHEWQALQPQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVR
NKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGLQVINGLNSTEPLVKEYAAFVLGA
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKVLFALCSLLRHFPYAQRQFLKLGG
LRTLVQEKGTETVELAVRVVTLLYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPGLWEQGW
CEITAHLLALPEHDAREKVLQTLGVLLTCRDYRQDPQLGRTLASLQA
DEGYFQELLGSVNSLLKELRYQVLASLELQDGE

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 455

CCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAGT
GGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCCTA
CCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT
CTGTGCGTCCTGCACCCACATCTTCTCTGTCCCCCTCCTGCCCTGTCTGGAGGCTGCTAGAC
TCCTATCTTCTGAATTCTATAGTCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCTTG
TGGTTCCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATGG**CTACAGCAAGACCCCCCTGGA
TGTGGGTGCTCTGTGCTCTGATCACAGCCTGCTTCTGGGGGTACAGAGCATGTTCTGCCA
ACAATGATGTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG
GAGCTGGGGCGGGGAAGACGCCCGTCGGATGACAGCAGCAGCCGATCATCAATGGATCCG
ACTGCGATATGCACACCCAGCCGTGGCAGGCCCGCCTGTTGCTAAGGCCAACAGCTCTACT
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTACGCCGCCACTGCAGGAAGAAAGTTT
TCAGAGTCCGTCTGCCACTACTCCCTGTCACCAGTTATGAATCTGGCAGCAGATGTTCC
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGCCACTCTAACGACCTCATGC
TCATCAAACACTGAACAGAAGAATTGTCCTCACTAAAGATGTCAGACCCATCAACGTCTCCTCTC
ATTGTCCTCTGCTGGACAAAGTGCCTGGTGTCTGGCTGGGACAACCAAGAGCCCCAAG
TGCACTTCCCTAAGGTCCCTCAGTGCTGAATATCAGCGTCTAAGTCAGAAAAGGTGCGAGG
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTACAAAGCAGGTAGAGACT
CCTGCCAGGGTGATTCTGGGGGGCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCC
GGGGAGATTACCCCTTGCCCGGCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA
CCAAGTGGATCCAGGAAACCATCCAGGCCACT**TGAG**TCATCCCAGGACTCAGCACACCGG
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTCAGACCCCTATTCCCTCAGAGA
TGTTGAGAATGTCATCTCCAGCCCTGACCCATGTCCTGGACTCAGGGTCTGCTTCC
CCCACATTGGCTGACCGTGTCTCTAGTTGAACCTGGAACAAATTCCAAAATGTCCAG
GGCGGGGGTTGCGTCTCAATCTCCCTGGGCACCTTCATCCTCAAGCTCAGGGCCATCCCTT
CTCTGCAGCTTGACCCAAATTAGTCCCAGAAATAACTGAGAAGTGGAAAAAA

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FIGURE 456

MATARPPWMWVLICALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLTAACRKVFVRVRLGHYSLSPV
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPASAGTKCLVSG
WGTTKSPQVHFVFKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSQGDGGPVVCN
GSLQGLVSWGDPYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 457

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGAAAGAACATTAGGAATGCCTTTAGTGCCTTGCTTCCTGAAC
AGCTCACAGTAGCCCGGCGCCCAGGCAATCCGACCACATTCACTCTCACCGCTGTAGGAATCCAGATGCAGG
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG
CCACAACCTCGGCATCCAGAGCCCCGGCCACAGAGCACAGGGCTCCCTCTCAACGTGGCGACCAGTGGCCCTGA
CCCTGCTGACTTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTCAGTACTACCAGC
TCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAGATTAGGAATACGTCCAAGAGTTGCAATCTC
TTCAAGTCCAGAAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAACTCTGTCGTGAGCTGTATAACA
AAGCTGGAGCACACAGGTGCAGCCCTGTACAGAACATGGAATGGCATGGAGACAATTGCTACCAGTTCTATA
AAGACAGAAAAGTTGGGAGGACTGTAAATATTCGCCTTAGTGAAACTCTACCATGCTGAAGATAAAACAAAC
AAGAAGACCTGGAATTGCGCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTTTGCGCC
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACCTCTGAACGTGTTCCATATTATAATAGATG
TCACCAGCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGATGATCTCTCAAAGGACTGCAAAGAATTGA
AGCGTTGTGCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCATGTCCTTGTGAAACATTAGGCG
AAGGTGACTGATTGCCCTGCAACTACAAATAGCAGAGTGAGCCAGGCAGGTGCCAAAGCAAGGGCTAGTTGAG
ACATTGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGTTCTCGTGTTCCTGTT
CAGGATCACCAGCATTCTGAGCTGGGTTATGCACGTATTAAACAGTCACAAGTCTTACATGCCAC
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTCTGGCTTAGAGATAACTTTAGCTCTTTCTCTCAA
TGTCTAATATCACCTCCCTTTCATGTCTCCTACACTTGGTGAATAAGAAACTTTGAAGTAGAGGAAA
TACATTGAGGTAACATCCTTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTAC
CAGCAAATACACAAGGAATTCTTTGTTCAAGTCATACTAGTCCCTCCAAATCCATCAGTAAGACCC
CATCTGCCCTGTCATGCCCTTCCAAACAGGGATGTCACCTGATATGAGAATCTCAAATCTCAATGCCCTATAA
GCATTCCTTCTGTGTCATTAAGACTCTGATAATTGTCTCCCTCATAGGAATTCTCCAGGAAGAAATAT
ATCCCCATCTCCGTTCATCAGAAACTACCGTCCCCGATATTCCCTCAGAGAGATTAAAGACCAGAAAAAGT
GAGCCTCTCATCTGCACCTGTAATAGTTCAAGTCCATTGACCCATATTATACCTTCAGGT
ACTGAAGATTTAATAATAATGAAATACTGTGAAAAA

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FIGURE 458

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLTCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGILLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEI
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 459

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCAC
TGGCGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCTGT
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT
CAGCTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAAGCAGGGAA
GTGGGAGCCTCGAGCCCTCGGGTGGAGCTGACCCAAGCCACCCCTCACCTGGACAGGAATGA
GAGTGTCAAGGTGTGCTCGCCTCCCTGGCCCTCATCTTGCCATAGTCACGACATGGATGTTA
TTCGAAGCTACATGAGCTTCAGCATGAAAACCACCGTCTGCCACGCTGGCTGGCAGCCTCGC
CCACCAAGGAGATCCAGGTTAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAAC
ACTTTGCGTTAAAATCTGCAGTGGGCCGCAACGTCGTGGCCCTACTATGTGCTTGAAAG
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATGCCCTGGTGA
ATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGGAGATGTTATGC
ACCTAGTGAAATTCCCTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGGCCTACGACG
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGGAGTTCCCTACG
CAAACAAACTGGGCTTCCGGGACAGCTGGTCTTCATAGGAGCCAAGACCTCAGGGTAAAA
GCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACGAGGGATGCCAGAGC
TGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATTTAGGGTGGCTGTGGCTTCCCTCAG
CCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCGGCAGGGCTGAGGAGGA
GGAGCAGGGGTGCTGCGTGGAGGTGCTGCAGGTCCCTGCACGCTGTGTCGCGCCTCTCCTC
CTCGAAACAGAACCCCTCCCACAGCACATCCTACCCGAAGACCAGCCTCAGAGGGTCTTCT
GGAACCAGCTGTGAGAGAATGGGGTGTTCGTCAAGGACTGCTGACGGCTGGTCTG
AGGAAGGACAAACTGCCAGACTTGAGCCAATTAAATTTATTTGCTGGTTTGAAAAAA
AAAAAAAAAAAAAA

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FIGURE 460

MRVSGVLRLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFDLGSSYAKQLGFRDSWVFIGAKDLRG
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 461

AAACTCAGCACTTGC~~CCGG~~AGTGGCTATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA
AACCTGAGCGGTGAGACTCCCAGC~~T~~GCTACATCAAGGCC~~C~~CAGGACATGCAGAACCTCCTC
TAGAACCCGACC~~A~~CCCCACCAATGAGGTCTGCCTGGAGATGCAGGCACCTGAGCCAAGGCGT
CCAGTGGCCTTGCTTCTGGCTGTCTGGCTTCTTCTCTTCGCCTGCCCTCTTTATTAA
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA
GTC~~CC~~CTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACACC~~A~~TATGCAGA
GCCAGCGCCAGAGAACAA~~T~~GCCTCAACACACAAACCCAGCCAAGGCCACACCACGGAGA
CAGAGGAAAGGAGGCCACCAGGCACCAGGCCAGGAGCAGGACAAGGTGCCACACAGCACA
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACC~~A~~TGGTGAACACACTGTCA~~CC~~CAGAGG
GCAAGATGCAGGGATGCCCTCTGGCAGGACAGAGGCACAA~~T~~CATGGAAGAGGCCAGGACACAAA
GACGACCCAA~~G~~GAATGGGGCCAGACCAGGAAGCTGACGGC~~T~~CCAGGACGGTGT~~C~~AGAGAA
GCACCAGGGCAAAGC~~G~~GAACCACAGCCAAGACGCTCATTC~~C~~AAAAGTCAGCACAGAATGCT
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGT~~G~~ACCACAGCAGTCATCCC
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTCCAGAGGCCACGAGCA
GAGAAACCAAAAGACTGAAGGCCCAACTTCAAATCTGAGC~~T~~CTGGTGGGATT~~T~~GAGGAAAA
ATACAGCTT~~C~~GA~~A~~ATAGGAGGCC~~T~~CAGACGACTTGCCTGACTCTGTGAAGATCAAAGCCTC
CAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTCTT~~C~~GGACTCCAGACA
CTTCAACCAGAGT~~G~~AGTGGGACCC~~T~~GGAACACTTGCACCA~~C~~CC~~T~~GGCTT~~C~~ATGGAGCT
CAACTACTCCTTGGTGCAGAAGGT~~C~~GTGACAGC~~T~~CC~~C~~CTCAGT~~G~~CC~~C~~CAGCAGC~~G~~GT~~C~~
CCTGGCCAGC~~C~~CTCCCC~~G~~TGGAGC~~C~~CTCCGGTGCATCACCTGTGCC~~G~~GTGGCAACGGGG
CATCCTGAACAA~~C~~CTCCACATGGCCAGGAGATAGACAGTCAGACTACGTGTTCCGATTGAG
CGGAGC~~T~~CTCATTAAAGGCTACGAACAGGATGTGGGACT~~C~~GGACATC~~T~~CTACGGCTTAC
CGCCTTCTCC~~C~~TGACCA~~G~~GTCACTC~~T~~TATATTGGCAAT~~C~~GGGTTCAAGAACGTGCC~~T~~
TGGGAAGGACGTCCGCTACTTGCACTTCTGGAAAGGCACCCGGACTATGAGTGGCTGGAAGC
ACTGCTTATGAATCAGACGGT~~G~~ATGTCA~~A~~AAAAC~~C~~TTTCTGGTT~~C~~AGGCACAGACCCAGGA
AGCTTT~~C~~GGGAAGC~~C~~CTGCACATGGACAGGTACCTGTT~~G~~CTGCACCCAGACTT~~C~~CCGATA
CATGAAGAACAGGTTCTGAGGT~~C~~TAAGACCC~~T~~GGATGGT~~G~~CC~~C~~ACTGGAGGATATACCGCC
CACCACTGGGCC~~C~~CTCTGCT~~C~~ACTGCC~~T~~TCAGCTGTGACCAGGT~~G~~AGTGCTTATGG
CTTCATCACTGAGGGCCATGAGCG~~T~~TTCTGATCACTACTATGATA~~C~~ATGGAAAGC~~G~~GCT
GATCTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGT~~C~~TGGAAGCGG~~T~~ACACGAT~~G~~A
AGGGATAATCCGGCTGTACCAGCGT~~C~~CTGGT~~C~~CC~~G~~GA~~A~~CTGCC~~A~~AGCCAAGAACTGACCGG
GCCAGGGCTGCCATGGT~~C~~CTTGC~~C~~CTGCC~~A~~AGGCACAGGATA~~C~~AGTGG~~A~~TCTGAGAC
TCTTGGCCATT~~C~~CCATGGCT~~C~~AGACTAAGCTCAAGCC~~C~~CTCAGGAGT~~T~~CCAAGGGAAACAC
TTGAACC~~A~~GGACAAGACTCTCTCAAGATGGCA~~A~~ATGGCTAATTGAGGTTCTGAAGT~~T~~CTCA
GTACATTGCTGTAGGT~~C~~CTGAGGCCAGGGATT~~T~~TAAATTAA~~A~~ATGGG~~T~~GATGGGTGCC~~A~~ATA
CCACAATT~~C~~CTGCTGAAAAACACTTCCAGT~~C~~AAAAGCTT~~C~~TGATACAGAAAAAGAGCC
TGGATT~~T~~ACAGAAACATATAGATCTGGTTGAATT~~C~~CAGATCGAGTTACAGTTGT~~G~~AA~~A~~TCT
TGAAGGTATTACTTAAC~~T~~CACTACAGATTGT~~C~~TAGAAGAC~~C~~TTCTAGGAGTTATCTGATT~~C~~
TAGAAGGGTCTATACT~~T~~GT~~C~~CTGT~~T~~TAAGCT~~T~~TGACA~~A~~CT~~T~~ACGT~~G~~T~~T~~GTAGAAAAC
TGATAATAATACAA~~A~~ATGATTGTTGCCATGGAAAGGCAAATAAAATT~~T~~TCTACAGT~~G~~AAAAAAA
AAAAAAA

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FIGURE 462

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK
SQAPTRARRTTIYAEPAPEENNALTQTPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTAASRTVSEKHQGKAA
TTAKTLIPKSQHRLMLAPTGAWSTRTRQKGVTAVIPPKEKKPQATPPPAPFQSPTTQRNQLRK
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRFNQSEW
DRLEHFAPPFGFMELNYSLVQKVVFTRPPVPQQQLLLASLPAGSLRCITCAVVNGGILNNSH
MGQEIDSHDYVFRSGALIKGYEVDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVPLGKDVR
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFLRYMKNRFL
RSKTL'DGAHWRIYRPTTGALLLTALLCDQVSAYGFITEGHERFSDHYYDTSWKRLIFYINH
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Important features:**Cytoplasmic Domain:**

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 463

GGGGGAGCTAGGCCGGCGCAGTGGTGGCGGCGCAAGGGTGAGGGCGGCCAGAAC
CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTCTCCCTCAAATGGTCCCTTGCACCATGTC
ATTCTACTTTCTCACTGTTGGCTCTTAACCTGTGTCACCTCCTCATGGTGTCAAGAGCAC
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTCTTGGAAATAAAATCAGACTTCTGA
GTACGTCACTCCAGTTCAATTATGATCTCTGATCCATGCAAAACCTTACACGCTGACCTTCTG
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAAGCACCATCATCCTGCATAGTCA
CCACCTGCAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAAC
CCTGCAGGTCTGGAAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCGAGCCCCCTCCT
TGTGGGCTCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTCGGAGACTTCCACGG
ATTAAACAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGATACTAGCATCAACACAATT
TGAACCCACTGCAGCTAGAATGCCCTTCCCTGTTGATGAACCTGCCTCAAAGCAAGTT
CTCAATCAAATTAGAAGAGAGCAAGGCACCTAGGCATCTCAATATGCCATTGGTGAATC
TGTGACTGTTGCTGAAGGACTCATAGAACCAATTGATGCACTGTGAAGATGAGCACACTA
TCTGGTGGCCTTCATCATTCAAGATTGAGTCTGTCAGCAAGATAACCAAGAGTGGAGTCAA
GGTTCTGTTATGCTGTGCCAGACAAGATAAAATCAAGCAGATTATGCACTGGATGCTGCGGT
GACTCTCTAGAATTATGAGGATTATTCACTACCGTATCCCCTACCCAAACAAAGATCT
TGCTGCTATTCCCGACTTCAGTCTGGCTATGGAAAAGTGGGACTGACAACATATAGAGA
ATCTGCTCTGTTGATGCAAGAAAAGTCTCTGCACTCAAGTAAGCTGGCATCACAGTGAC
TGTGGCCCAGTGAACCTGGCCACCCAGTGGTTGGGAACTGGCACTATGGAATGGTGGAAATGA
TCTTGGCTAAATGAAGGATTGCAAAATTATGGAGTTGTCAGTGTGACCTGCACCCATCC
TGAACGTAAAGTGGAGATTATTCTTGGCAATGTTTGACGCAATGGAGGTAGATGCTT
AAATTCCCTCACACCTGTGTACACCTGTGGAAAATCCTGCTCAGATCCGGGAGATGTTGA
TGATGTTCTTATGATAAGGGAGCTTGTATTCTGAAATATGCTAAGGGAGTATCTAGCGCTGA
CGCATTAAAGTGGTATTGTCAGTATCTCAGAACGATAGCTATAAAACAAAAACGA
GGACCTGTGGGATAGTATGGCAAGTATTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT
TTGCTCTAGAAGTCAACATTCACTTCCATCCTCACATTGGCATCAGGAAGGGGTGGATGTA
AACCATGATGAACACTGGACACTGCAAGGGGTTTCCCTAAATACACATCACAGTGAGGG
GAGGAATGTACACATGAAGAACGACTACATGAAGGGCTTGACGGCGCCCCGGACACTGG
GTACCTGTGGCATGTCATTGACATTCACTACAGCAAATCCAACATGGTCCATCGATT
GCTAAAAACAAAAACAGATGTGCTCATCTCCAGAAGAGGTGGAATGGATCAAATTAAATGT
GGCATGAATGGTATTACATTGTCATTACAGGAGTGTGGACTCTTGACTGGCCT
TTTAAAGGAACACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAAACATGCATT
TCAGCTCGTCAGCATTGGGAAAGTGTCCATTGAAAAGGCTGGATTATCCCTGTACTGAA
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTGAATGAGCTGATTCTATGTATAAGTT
AATGGAGAAAAGAGATATGAATGAAGTGGAAACTCAATTCAAGGCTCTCATCAGGCTGCT
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG
GAGTGAACACTACTCTCGCCCTGTGTGACAAACTATCAGCCGTGCGTACAGAGGGCAGAAGG
CTATTTCAGAAAAGTGGAGGAAGTCAAATGGAAAAGTGTGAGCTGGCTGTGACGTGACCTGGC
AGTGTGCTGTGGGGCCCAGAGCACAGAAGGCTGGGATTTCATAGTAAATATCAGTT
TCCTTGCTCCAGTACTGAGAAAAGCCAATTGAATTGCCCTCTGCAGAACCCAAAATAAGGA
AAAGCTCAATGGCTACTAGATGAAAGCTTAAGGGAGATAAAATAAAACTCAGGAGTTCC
ACAAATTCTACACTCATTGGCAGGAACCCAGTAGGATACCAACTGGCCTGGCAATTCTGAG
GAAAAACTGGAACAAACTTGTACAAAAGTTGAACCTGGCTCATCTCCATAGCCCACATGGT
AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAAGAGGTAAAAGGATTCTTCAG
CTCTTGAAAGAAAATGGTTCTCAGCTCCGTGTGTGCAACAGACAAATGAAACCCATTGAAGA
AAACATCGGTTGGATGGATAAGAATTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAAGCT
TGAACGTATGAAAAATTCCCTCCCTGGCCGGTTCTGTTGAGTAAATCTCTAATCACCAACATT
TGAGTGTATTTCAAAATAGAGATGGCTGTTGGCTCCAAGTGGAGATACTTTTCCCTC
AACTCATTTTGACTATCCCTGTGAAAAGAATAGCTGTTAGTTTGTCAATGAATGGCTTTT
CATGAATGGCTATCGCTACCATGTGTTGTCATCACAGGTGTTGCCCTGCAACGTAAACC
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAGTACCTTATTCTCTCAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 464

MVFLPLKWSLATMSFLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY
DLIHNLTTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP
PQEIQIALLAPEPLLVLGPYTVVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM
AFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDTVKMSTYLVAFIIS
DFESVSKITKSGVKVSYYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAAIPDFQ
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNIVTMEMWWNDLWLNEGF
AKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDMSASICPTDGVKGMGFCRSQHS
SSSSHWHQEGDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSAPDTGYLWHVPL
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTLKGHTA
VSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRDMN
EVETQFKAFIRLLRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALCRTQNKEKLQWLLD
ESFKGDKIKTQEFPQILTIGRNPVGYPLAWQFLRNWNKLVQKFELGSSIAHMVMGTTNQF
STRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIRVWLQSEKLERM

Important features:**Signal peptide:**

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 465

CAGCCACAGACGGGTCATGAGCGCGGTTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCACT
GCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGGACAGTTCAGCATGTGTGAAGGTGTCCGA
CCTACCCCCGGAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTGGGTGCCAGGACAC
GTTGATGCTCATTGAGAGCGGACCCAAGTGAGCACCCTGAGGATGGGCCCTCTCCCTGATCTCCTA
CAAGGACCAGGAGGCCCGCGTCACTGAGCACCGGATGGGCCCTCTCCCTGATCTCCTA
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCGCTTGGGC
CCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG
TCTGGAGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGATGGCCTCCT
CAGGCTCAGGGGAGGAGGCATCTCTCAATCTGAGAGTCCAGGGATGCATGCCAGGCCAGG
TTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGTATGACTGAGAACTGCAATAG
GAAAGATTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGTGTGTCAAGGAGAC
GCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAAGGCTGCAGCACTGT
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCTGGGTGCTTGTGGCCTC
CTATAACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCGTTCTGCTGAA
CTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCCCTACCTGTGTGCAGCC
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGGGCGCCACTCATTGTTA
TGATGGGTACATTCTCATCTCAGGAGGTGGCTGTCCACCAAAATGAGCATTCAAGGCTGCGT
GGCCAACCTCCAGCTTCTGTGAACCACACCAGACAAATCGGATCTTCTGCGCGTGA
GAAGCGTATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGCTGAGGGCCTGGAGTC
TCTCACTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGAGTGGTTGCCCTC
CTGCTAACTCTATTACCCCCACGATTCTCACCGCTGCTGACCACCCACACTCAACCTCCCTC
TGACCTCATAACCTAATGGCTTGGACACCAGATTCTTCCCATTCTGTCCATGAATCATCTT
CCCCACACACAATCATTCATATCTACTCACCTAACAGAACACTGGGGAGAGCCTGGAGCAGC
CGGACTTGCCTATGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATAACAGAC
CCTGTCCTTCA

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FIGURE 466

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTCDSGLCQDTIMLIE
SGPVSVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA
DPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNLLN
GTQEIGPGMTENCNRKDFLTCHRGTTIMHGNLAQEPTDWTSNTEMCEVGQVCQETLLLID
VGLTSTLVGTVKGCVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLNSLPQ
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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FIGURE 467

GAGGATTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTG
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTCAGGATGATGGTGCCTTCG
AGGAGCTCTGCATTGCTGGTTCTGTCAGCTTCTGCCCGCCGCAGTGTACCA
GGACCCAGCCATGGTGATTACATCTACCGCGCTTCGAGCTTGGAGCAAGGGCTGGAAAA
ATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATCTGT
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGAGTGGTAACCTGGCACT
GAGAGTTAACGTGCCAACGGGAGATTGACTACATACAATACTTCAGAGGGCTGACGAGTG
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCAAGAAGCTGAAGAAGAGAAAA
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTGAAAAT
AGTGAAGAAGATGATGGACACACATGGCTTGGATGAAAGATGCTGTCTATAACTCTCAA
GGTGTACTTATTAATTGGATCCAGAAACAACTGTTGGGAAATTGCAAACATACGGGCATT
CATGGAGGATAACACCAAGCCAGCTCCCCGAAGCAAATCTAACACTTCCCTGGCAGGGAAC
AGGCCAAGTGAATCACAAGGTTTCTATTTCATAACCAAGCAACTCTAACATGAGATAAT
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCAGGGGGTAGGCCG
AGCATTGGTTTACCAAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT
CTGGGCCATCCACTCTGGGCAGGCACCCATAGCCATTGGTCTCACAAAGATTGAGCCGGG
CACACTGGGAGTGGAGCATTGATGGGATAACCCATGCGAGAAGCCAGGATGCTGAAGCCTCATT
CCTCTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCAGGGCCCTATCGCATCAC
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGACTTGCCTAACATTGTTCTCCCCAA
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCCTGGAA
TGAAGGAAACAGATCATTTACAACACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAAATGCAT
TACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC
CCCTTCACAATATAGTATCCCTCTAACACACAGGAAGAGTGTTAGAAGTGGAAATACGT
ATGCCCTCTTCCAAATGTCACTGCCTTAGGTATCTTCAAGAGCTTAGATGAGAGCATATC
ATCAGGAAAGTTCAACAATGTCATTACTCCCCAAACCTCTGGCTCTCAAGGATGACCAC
ATTCTGATACAGCCTACTTCAGCCTTTGTTACTGCTCCCAGCATTACTGTAACTCTG
CCATCTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCTAACATTCAACACTGGCTTTCTC
TCCCCCTGGCTTTGCTGAAGCTCTCCCTTTCAATGCTATTGATATTCTCCCATT
CACTGCCCAACTAAATACTATTAAATATTCTTCTTTCTTTGAGACAAAGGT
CTCACTATGTTGCCAGGCTGGCTCAAACCTCCAGAGCTCAAGAGATCCTCTGCTCAGCCT
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTAAATACTATTCTTATTG
AGGTTAACCTCTATTCCCTAGCCCTGCTTCACTAACGTTGGTAGATGTAATAATAAA
GTGAAAATATTAACATTGAATATCGCTTCCAGGTGTGGAGTTGCACATCATTGAATT
TCGTTTCACCTTGTTGAAACATGCACAAGTCTTACAGCTGTCATTCTAGAGTTAGGTGAGT
AACACAATTACAAAGTGAAGAGATACAGCTAGAAATACTACAAATCCCTAGTTTCCATTG
CCCAAGGAAGCATCAAATACGTATGTTGTCACCTACTCTTATAGTCATGCGTCATCGTT
TCAGCCTAAATAATAGTCTGTCCTTTAGCCAGTTCTAGTCTGCACAAGACCTTCAT
AGGCCTTCAATGATAATTCCCTCAGAAAACCAGTCAAGGGTGAGGACCCAACTCTAGCC
TCCTCTGTCTGCTGCTCTGTTCTCTCTGCTTAAATTCAATAAGTGACACTG
AGCAAAAAAAAAAAAAAA

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FIGURE 468

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQEF
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRREIDYIQYLREADECIVSEDKTLAEMLLQE
AEEEKKIRTLLNASCDNMLMGIKSLKIVKKMDTHGSWMKDADVNSPKVYLLIGSRNNNTVWEF
ANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMILL
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKIEPGTLGVEHSWDTPCRSQ
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK
QLYAWNENQIIYKLQTKRKLPLK

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FIGURE 469

TGGCCTCCCCAGCTTGCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC
AGTGTGTTGCCTTCACCCCAAGTGACCATGGAGAGGTGCCACCGAGTCTCAATCATGCTCCTC
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTCGAGGGCTGCGGATGTGCACCCGCTGGG
CGGGAAAGGCAGGGAGTGCCACCCGGCAGCCACAAGGTCCCCTTCAGGAAACGCAAGCAC
CACACCTGTCCCTGCTGCCAACCTGCTGTGCTCCAGGTTCCGGACGGCAGGTACCGCTGC
TCCATGGACTTGAAGAACATCAATTTAGGCCTGCCTGGTCTCAGGATAACCACCATCCT
TTTCCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCATGACTCTCCAG
TCCCTACACTGACTACCCCTGATCTCTCTGTCTAGTACGCACATATGCACACAGGCAGACATA
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG
AAAGGTGGCCAGCCTGGTTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA
GGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTTTCTGGCCCTGCCCTCTCCCCA
CATGTATCCCTCGGTCTGAATTAGACATTCCCTGGGCACAGGCTCTGGGTGCATTGCTCAGAG
TCCCAGGTCTGGCTGACCTCAGGCCCTCACGTGAGGTCTGTGAGGACCAATTGTGGT
AGTCATCTCCCTCGATTGGTTAACCTCTTAGTTCAGACCAACAGACTCAAGATTGGCTCTT
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCAGGGAGGCCAATCAGCC
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTCTGCCA
GAATTGTCATGCCCTGAGGCCCTCTTACACACTTACAGTTAACCACTGAAGCCCCCA
ATTCCCACAGCTTCCATTAAAATGCAAATGGTGGTGGTCAATCTAATCTGATATTGACAT
ATTAGAAGGCAATTAGGGTGTTCCTAAACAACTCCTTCCAAGGATCAGCCCTGAGAGCAG
GTTGGTGACTTGTAGGAGGGCAGTCCTGTCCAGATTGGGTGGGAGCAAGGGACAGGGAGC
AGGGCAGGGCTGAAAGGGCACTGATTGACCAAGGGAGGCAACTACACACCAACATGCTGG
CTTGTAGAATAAAAGCACCAACTGAAAAAA

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FIGURE 470

MRGATRVSIMLLLTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHPG
SHKVPFFRKHKHTCPCLPNLLCSRFPDGRYRCSDILKNINF

Important features:**Signal peptide:**

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 471

AGCGCCGGCGTCGGGCGGTAAAAGGCCGCAGAAGGGAGGCACTTGAGAAATGTCTTCC
TCCAGGACCCAAGTTCTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGCTG
CTGCCTGGCATTGCTGCTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGGCC
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAAAGCAA
AGGAGCTATGGAAAAAAATGGAGCTGTGATTATGCCGTGCGAGGCCAGGCTGTTCCCTCT
GTCGAGAGGAAGCTCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGCGTCCCC
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTTATTCAAAG
GAGAAATCTTCCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTA
TGGGATTTATCCGTCTGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAGGCTCTCTG
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGAGTTTCTGGTGGGATCAGGAAAGCAGG
GCATTCTTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACTTCTGTTCTGG
AAGCTGCTAAGATGATCAAACCACAGACTTGGCCTCAGAGAAAAAATGATTGTGTGAAACTG
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTCATGGATGTATTGTTCCACTCGT
TCCCTAAGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTATTAATGTATTTAA
TATTCTGTTAGGCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAAA
CTAATGAGGATTATTAAGCTAAAACCTGGAAATAGGAGGCTAAAATTGACTGCCAGGCTGG
GTGCAGTGGCTCACACCTGTAATCCCAGCAGCTTGGGAGGCCAAGGTGAGCAAGTCAC TGAG
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTCTCTACTAAAAATACAAAA
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCGGGAGGCTGAGGCAGGAGAA
TCACTTGAACCTGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG
GGTGAUTGAGACTCTAACTAA

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FIGURE 472

MSFLQDPSFFTGMWSIGAGALGAAALLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT
FKAHELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP
YFKGEIFLDEKKKFYGPQRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGFILGGVFVVGS
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 473

AATATATCATCTATTATCATTAAATAATGTATTCTTTATTCCAATAACATTGGGTTT
TGGGATTTAATTTCAAACACAGCAGAATGACATTCTGTCACTATTATTATTGTTGGT
ATGTGAAGCTATTGGAGATCCAATTCAAGGAAGCAACACATTGGAGAATGGCTACTTCTATC
AAGAAATAAAGAGAACACCACAGTCACCCACACAATCATCTTAGAAGACAGTGTGACTCCTAC
CAAAGCTGTCAAACACAGGCAAGGGCATAGTTAAGGACGGAATCTTGAUTCAAGAGGGTT
AATTCTTGGTGCTGAAGCCTGGGCAGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA
AATTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCAATATACAA
TAAGGTGAAATTATAAGTACCCATGCAGTTGGCTGGACAGTTCTAAATTGGACTTATTAAT
TTTAAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT
TTGATACAAATAAAAGAAAAGTGTCTCTCCCCTACAGAATTGACATTAAATGCGATACA
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA
TGTTGCCAAGGAAAAAA

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FIGURE 474

MTFFLSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG
IVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 475

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCAT
CTCCCACCGAGAGTCATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCCTC
AGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGCATG
CAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCTGAAG
CCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCAAGGTGCTCAGC
GATGCTGGACACAAGGTCAACCATCCTGGAGGCAGATAACAGGATCGGGGCCATCTTCACC
TACCGGGACCAGAACACACGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAGCTCTCAC
AGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTTCACCCAGTACGAC
AAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAGAAGGTGCC
GAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGGCACTCGCCCGAAGACATCTACCAAG
ATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGGCATGAAGAAG
TTTGAAAGGCACACGCTCTTGGAAATATCTCTCGGGAGGGAACCTGAGCCGGCCGGCGTG
CAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTATCTCAGCTCGCCGAGGCCCTC
CGGGCCCACAGCTGCCCTCAGCAGACTCCAGTACAGCCGATCGTGGGTGGCTGGACCTG
CTGCCGCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAACGCGCCGTGGTGGCG
ATGACCCAGGGACCGCACGATGTGCACGTGAGACATCGAGACCTCTCCCCGGCGCGGAATCTG
AAGGTGCTGAAGGCCGACGTGGTGTGTCGACGGCGAGCGGACCGCGGTGAAGCGCATCAC
TTCTCGCCGCCGCTGCCCGCCACATGCAGGAGGCCTGCGGAGGCTGCACACTACGTGCCGCC
ACCAAGGTGTTCTAAAGCTTCCGAGGCCCTCTGGCGCGAGGAGCACATTGAAGGCAGGCCAC
TCAAACACCGATGCCCGTCGCCATGATTCTACCCGCCGCCGCGAGGGCGCTGCTG
CTGGCCTCGTACACGTGGTGGACGCCGGCAGCGTTGCCGGCTTGAGCCGGGAAGAGGCG
TTGCCCTGGCGCTCGACGACGTGGCGCATTGCACGGCCTGTCGTGCCAGCTCTGGAC
GGCACCGCGCTGTCGAAGCGTTGGCGAGGACAGCACAGCCAGGGTGGCTTGTTGACAG
CCGCCGGCGCTGGCAAACGAAAAGGATGACTGGACGGTCCCTATGCCGCATCTACTTT
GCCGGCGAGCACACGCCCTACCCGACGGCTGGTGGAGACGGCGGTCAAGTCGGCGCTGCC
GCCGCCATCAAGATCAACAGCCGAAGGGCCTGCATCGGACACGCCAGCCCCGAGGGCAC
GCATCTGACATGGAGGGCAGGGCATGTGCATGGGTGGCCAGCAGCCCCTGCATGACCTG
GCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGGCCAGTTATCTCTCAAAACACGACCCAC
ACGAGGACCTCGCATTAAAGTATTTGGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

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FIGURE 476

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRVI
VVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGIFTYRDQNTGWIGELGAMRMPSSHRLHK
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMALNQ
ALKDLKALGCRKAMKKFERHTLLEYLLGEGLNSRPAVQLLGDMSEDGFYLSFAEALRAHSC
LSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA
DVVLLTASGPRAVKRITFSPLPRHMQEALRRLYVPATKVFLSFRRPFWREEHIEGGHSNTDR
PSRMIFYPPPREGALLLASYTWSAAAAFAGLSREEARLALDDVAALHGPVVRQLWDGTGVV
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI
NSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQNTTHRTSH

Important features:

Signal peptide:

amino acids 1-21

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FIGURE 477

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTCTGCCTGCCAT
GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCACGAGCGAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACTCAGAGCCGGAAAGCCCCATTCACTAGAACGACTGAGAGATCGGCCCTCGCAGGGCTCTGAATTCT
GCTGCTGTTCACAAAGATGCTTTATCTTAACCTTTGTTTCCCACCTCCGACCCGGCCTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTCTTGCTGATCACCAGACCTCAACCGTCTTACCTCTTGACCTGAA
CAATCAGTCTGTTGGAAATTGAGGGAGGAGCACGGAAGGGGTTTCCCAGAAGAACATGACCTAACAAAGTGTG
CTTCTCAGATGCCAAGACTATGTTGAGGTTTCAAAGAGGACTCGCTGCTGACAATGGGCCCTGTTGGG
ATATAGAAAACCAACAGGCCCTACAGATGGCTATCTAACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT
CTGTCCTG
GATCATCTCGAATTGGCTTACACGTTACTCTATGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CATCGTACATATTGTCACAAAGGCTGATATGCCATGGTGTGACACACCCCCAAAGGCATTGGTGTGATGAC
AGGGATGTTGAGAGAAGGCTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGATGATGACCTGAA
GCAAAGAGGGAGAAGAGTGGATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG
AAAACCTGTGCTCTTAGCCAGAACGACTGAGCGTCATCTGCTTCACCAAGTGGGACCACAGGTGACCCCAAAGG
AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCTTCTCAAATGTTGAGAGGATTGTACAGGCTGTTGT
CACTCCTGATGATGTTGGCCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGT
CAGCTGAGGCCAGAGTGGATTCTCCAAGGGGATATTGCTGCTGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTCCCGCGGTGCCTGACTCCTAACAGGATCTACGATAAGGTACAAATGAGGCAAGACACCCCT
GAAGAAGTTCTGTTGAAGCTGGCTTCCAGTAATCAAAGAGCTCAAAGGGTATCATCAGGATGATAG
TTTCTGGGACAAGCTCATTTGCAAAGATCCAGGACAGCCTGGCGAAGGGTCTGTAATTGTCACTGGAGC
TGCCCCCATGTCACCTCAGTCATGACATTCTCCGGCAGCAATGGGATGTCAGGTGTTGATGAAGCTTATGGTCA
AACAGAATGCAAGGTGGCTGACATTACATTACCTGGGACTGGACATCAGGTACGTTGGGTGCCCCCTGGC
TTGCAATTACGTGAAGCTGGAGATGTGGCTGACATGAACTACTTACAGTGAATAATGAAGGGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAGGATACCTGAAGGACCCCTGAGAACAGACAGGAAGCCCTGGACAGTGTGGCTG
GCTTCACACAGGAGACATTGTCGCTGGCTCCGAATGGAACTCTGAAGATCATCGACCGTAAAAAGAACATT
CAAGCTGGCCAAGGAGAATACATTGACCCAGAGATAGAAAATATCTACAACAGGAGTCACCGTGTACA
AATTGTCACACGGGAGAGCTTACGGTACCTTAGGAGTGGTGGCTGACACAGATGTAATTCCCT
ATTTGCAAGCTTGGGTGAAGGGCTCTTGAGGAACGTGCTGCAAACCAAGTGTAAAGGAAGCCATT
AGAAGACTTGCAAGAAAATTGGAAAGAAAGTGGCTTAAACATTGTAACAGGTCAAAGCCATTTCATCC
AGAGCATTTCACATTGAAAATGGCTTGTACACCAACATTGAAAGCAAAGCAGGGAGAGCTTCCAAATACT
TCGGACCCAAATTGACAGCCTGATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCACTG
TGCACGTGCTGAGAAAATGGATTAAAATCTTACATTGTTGCTTCCCTATTTTTTAAC
TGTTAAACTCTAAAGCCATAGCTTTGTTTATATTGAGACATATAATGTTAAACTAGTCCAAATAATCA
ATCCGTCTTCCATCTCGATGTTGTAATATTAAGGCTTCAGGGCTACTTTATCAACATGCCGTCTCAA
GATCCAGTTATGTTCTGTCCTCCTCATGATTCTAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCTCTGTGCTCTTCTTGTGATAAACATAACTGCCAACAGTCTATGCTTATTACA
TCTTCACTGTTCAAACTAAGAGATTAAAATCTGAAAAACTGCTTACAATTCTAGTTCTAGCCACTCCAC
AAACCACTAAAATTAGTTAGCCTACACTCATGTCATATCTATGAGACAAATGCTCCGATGCTTT
CTGCTAAATTAAATTGTTAGCTACTGAAGGGAAAAGTTGATCATACCAAAACATTCTCAAACCTCTAGTTAGATA
TCTGACTTGGGAGTATTAACCTGGCTATGACATACTGTCACAGTTGCTGCTGAGCTGGAAGGAGTTGACA
CAGTAGGAACGGGGAGTAATGTTCCAGTAATGAAGCAAGCAACTGAATAAAACCTCTGAACTGGAAACAAAGATCT
GGTGGGCCAGTGAACCTTCCAGTAATGAAGCAAGCAACTGAATAAAACCTCTGAACTGGAAACAAAGATCT
ACAGGGCAAGCAAGATGCCACACAACAGGCTTATTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT
AGAGTCTGCTCTACCTACCCACAGATAACACATGTTGTTCTACTTGAAATGTTAAAGTCTTAAATAAC
TATTACAGATAAAAAAA

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FIGURE 478

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLFTKMLFIFNF
LFSPLPTPALICILTGFAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTSCC
FSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ
FVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG
NVEKGFTPSSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC
FTSGTTGDPKGAMITHQNIVSAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC
GARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE
LQKGIIRHDSFWDKLIFAKIQDSLGGRRVVIITGAAPMSTSVMFFRAAMGCQVYEAYGQTEC
TGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDP
QEALDSDGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVH
GESLRSSLVGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKESGLKT
VKAIFLHPEPFSIENGLLPTLAKRGELSKYFRTQIDSPLYEHQD

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGGCGGAGGCCGCAGCAGCCGGCCGAGCAGTGAGGGCCCTAGCGGGGCCAGCGGGGC
CCGGGGCCCTAAGCCATTCTGAAGTCATGGGCTGCCAGGACATTGGTGACCCGCCAATCC
GGT**A**TGGACACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGCTCGGAAGAACGGAGC
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
GGGGCCGTGCTTTCTGCTGGTACTGTCATTGTCAATATCAAGTTGATCCTGGACACTCG
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGCTCTGGACGTAGAGGT
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACACGGTGCCTGGAGGATGAGGCC
GAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGGCACGTGATGGCA
CGTGTGTTGACACGTACTCACCATGAGGATGAGGCCATGGTCTATTGTCACATGGTA
GCGCCCGGCCAGTGCTCATCTGCACTGTCAGGATGAGGCCCTTCCACCTCAAGGACA
GCCAAGGCTCTGCTGAGGAGCCTGGCAGGCCAGGCTGGCCCTGCCCTGGCTGGAGGGAC
TGGCCTTCTGGGACGAAAAGGAGGTCTGTCTCGGGAGAACATTCTAAGTCACCTGCC
CTCTCTCCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAACAG
GCAGAGTGCCTACTGGCAGACACAGAGCTGAACCGTCGCCGGCGCTCTGCAGCAAAGTT
GAGGGCTATGGAAGTGTATGCAAGGACCCACACCCATCGAGGTCAGCCCTGACCCA
CTCCCAGACAACAAGGCTCAATGTCCTGTGGCTGTCTATTGCAAGGAACCGACCCAA
CTGTCAGGATGCTGCCTCTGCTTCAGCCCAGGGGTGTCTCAGATGATAACAGTT
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTGGTCTGAGGGC
CAGCATACTCCATCAGCATCAAGAATGCCCGTGTCTCAGCACTACAAGGCCAGCCT
GCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTCTGGAAGAGGACCTGGAC
GCTGTGGATTTTCAGTTCTGAGCCAATCCACCTACTGGAGGAGGATGACAGCCTG
TACTGCATCTCTGCTGGAATGACCAGGGTATGAACACACGGCTGAGGACCCAGCA
TACCGTGTGGAGACCATGCCCTGGCTGGGTGCTCAGGAGGTCTTGTACAAGGAGGAG
CTTGAGCCAAGTGGCTACACCGAAAAGCTCTGGATTGGACATGTGGATGCCATGCC
GAACAAAGCCGGGGCCGAGAGTGCACTCATCCCTGACGTTCCGATCCTACCTGGC
GTCGGCCTAACATGAATGGCTACTTTCAGGCCACTTCAAGAACGACAAGTTCA
GTTCCAGGTGTCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTATGAAGTGG
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCTGTGAAGACT
CTGCCAGACACAGAGGCCACACCTACGTGGCTTATTCAATGGAGAAAGATGATGACT
ACCACCTGGACCCAGCTGCCAAGTGCCTCATATCTGGACCTGGATGTGCGTGGCA
CGGGGCCTGTGGAGATTGTTCGGAAGAAGAACACTCCCTGGTGGTGGGGTCCGGCT
CCCTACTCAGTGAAGAACCCACCTCAGTCACCCCAATTTCCTGGAGGCCACCC
GAGGGAGCCCCAGGAGGCCAGAACAGAC**TG**AACCTCCTCCAGGACCTGCGGGCT
ACTGTGTACCCCCAGGCTGGTAGCCCTTCCATCCTGTAGGATTGAGATGCTGGTA
GGGGCTGGGGCTACCTGTTTTAACATGAGACTTAATTACTAACCTCAAGGGAGGG
CTGCTCCAACACCCGTTCTGAGTTAAAGTCTATTATTACTCCTTGTGGAGAACGG
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTGA
TTCCAGGCCTGGCTCAGAATCTAACCTATTGACTGTCCTGAGGGCCTGAAA
CGAACCTGGAGGGCCTGGATTCTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCT
TTACTCAGGAAACTGCTGTGCCAACCCATGGACAGGCCAGCTGGGGCCACATG
AGACTCACTCAGAGACCCCTAGACACTGGACCCAGGCCCTCAGCCTCT
TTTCCAAAGCTGGATAAGTTGGTATTGATTTAAAAAGGAGAACGCC
CTGGAAAAAA
AAAAAAAAAAAAAA

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FIGURE 480

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTRR
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVYVAVDGTIVLEDEARE
QGRGIHVIVLNQATGHVMAKRVFDTYSYPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLKDTA
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPLLKDVPLOSSAEEA
ECHWADTELNRRRRFC SKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGNRPNYL
YRMLRSLLSAQGVSPQMITVFIDGYYEPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTA
TFNLFP EAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY
RVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKKEAYEVHRLLSEAEVLDHSKNPCEDSFL
PDTEGHTYVAFIRMEKDDDFTTWTLAKCLHIWDL D VRGNHRGLWRLFRKKNHFLVVGVGPASP
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 481

GAAAGAATGTTGGCTGCTTTTCTGGTACTGCCATTGCTGAACCTGTCAACCA
GGTGCAGAAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT
GCCTGGGATACCAATGAAGAATACCTCTCAAAGCGATGGTAGCTTCTCCATGAGAAAAGTT
CCCAACAGAGAAGCAACAGAAATTCCCAGTCCTACTTTGCAATGTAACCCAGAGGGTATCA
TTCTGGTTGTGGTTACAGACCCTCAAAAAATCACACCCCTCCTGCTGTTGAGGTGCAATCA
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTCTTCTAAATGACCAAACCTGGAA
TTTTAAAAATCCCTCCACACTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT
ATATTGGTGTGATATTTCATCATCATAGTTGCAATTGCACTACTGATTATCAGGGATC
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA
AACATGATCACAAATTGAAAATGGCATCCCCCTGTATCCCCCTGGACATGAAGGGGGCATATTA
ATGATGCCTCTGACCAGAGGATGAGAGGCTCACCCCTCTGAAGGGCTGTTGTTCTGCTTC
CTCAAGAAATTAAACATTGTTCTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT
CATATATTGTTCAACCATTCTCTTTGTAATAAATTGAAATGTGCTGAAAGTGAAAAG
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCAAGACTCAAATATTCTAA
AATATTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTGATTGATTAA
GCATTTTAGAAATAAGATCAGGCATATGTATATATTTCACACTCAAAGACCTAAGGAAAA
ATAAATTTCAGTGGAGAATACATATAATATGGTAGAAATCATTGAAAATGGATCCTTT
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA
AATGGATGGATAAAATGGAATTACTCATATACAGGGTGGATTTCACCTGTTATCACACCA
ACAGTTGATTATATATTTCTGAATATCAGCCCTAATAGGACAATTCTATTGTTGACCATT
TCTACAATTGAAAAGTCCAATCTGTGCTAACCTAATAAAGTAATAATCATCTTTTAAA
AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN
REATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL
KIPSTLAPPMDPSVPIWIIIIFGVIFCIIIVAIALLILSGIWQRRRKNEPSEVDDAEDKCENM
ITIENGIPSDPLDMKGIGLMMPS

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FIGURE 483

CGTCTCTGCCTCGCC**ATG**CGTCCCAGGGGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGC
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCATGGGCTGGGGAACCCCGCAGCCGGTGGTGT
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTCTCCAGACTGATGTCACCCG
GGCCGAGTGCTGTGCCTCCGGAACATTGACACCAGCCTGGTCCAACCTCACCCACCCGGGGAA
CAAGATCAACCTCCTCGGCTTGTGGCCTGTCCACTGCCTCCCTGCAAAGATTGTCAGA
CGGCGTGGAGTGCGGCCGGCAAGGCGTGCAGCCTGCTGGGGGCCGGCTGCGAGTG
CGCGCCGACTGCTCGGGCTCCCGCGCGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA
CCCGCAGCAGTGCGAGCTGCAGCCTGCGCTGCCCGGGCACAGTCGTGCGTGT
CCGGGGCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCGGGCACAGTCGTGCGTGT
GGACCCAGACGGGCAGCGCCCAGTGCCTGGTGTGAGCGGGGCCCTGCCCTGTGCCCTCCAG
CCCCGGCCAGGAGCTTGCGGCAACAACAACGTCACCTACATCTCCTGTCACATGCGCA
GGCACCTGCTTCTGGCCGCTCCATCGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCC
TGAGGAGCCGCCAGGTGGTGAGTCTGCAGAACAGAGGAAGAGAACATTGTC**TGA**GCTGCAGGAC
AGGCTGGCCTGGTGCCAGGGCCCCCATCATCCCCCTGTTATTATGCCACAGCAGAGTC
TAATTATATGCCACGGACACTCCTTAGAGCCCAGTCTGGGACACTTGGGATCCCAGAAC
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGCCGGCTGGTGGTGGGAT
AGACCTGCGTCCGGACACTGAGCGCCTGATTAGGGCCCTCTAGGATGCCCAAGCCCC
ACCCATAAGACCTATTGCCGGGAGGATTCCACACTTCCGCTCCTTGGGATAAACCTATTAA
TTATTGCTACTATCAAGAGGGCTGGCATCTCTGCTGGTAATTCTGAAGAGGCATGACTGC
TTTCTCAGCCCCAAGCCTCTAGCTGGGTGTACGGAGGGCTAGCCTGGGTGTACCGGA
GGGCTCTAGCCTGGGTGAGTACGGAGGGCTAGCCTGGGTGAGTACGGAGGGCTAGCCTGGG
GAGTACGGAGGGCTAGCCTGGGTGTATGGAGGGATCTAGCCTGGGTGAGTATGGAGGGCT
AGCCTGGGTGAGTATGGAGGGCTAGCCTGGGTGTATGGAGGGCTAGCCTGGGTGAGTAT
GGAGGGCTAGCCTGGGTGTATGGAGGGCTAGCCTGGGTGAGTATGGAGGGCTAGCCTG
GGTGTGACGGAGGGCTAGTCTGAGTGCCTGGGACCTCAGAACACTGTGACCTTAGCCC
AGCAAGCCAGGCCCTCATGAAGGCCAACAGAGGCTGCCACCATTCCCTGCCAGCCAAAGAACT
CCAGCTCCCCACTGCCTCTGTGTGCCCTTGCGCTGTGAAGGCCATTGAGAAATGCCA
GTGTGCCCTGGAAAGGGCACGGCCTGTGCTCCTGACACGGCTGTGCTGGCCACAGAAC
CACCCAGCGTCTCCCTGCTGTCCACGTCAGTTCATGAGGAACGTCGCGTGGTCTCAGA
CGTGGAGCAGCCAGCGGAGCTCAGAGCAGGGACTGTGTCCGGCGAGCCAAGTCCACTCTG
GGGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGTGTAGACG
CCAAGACTCACGCATGTGTGACATCCGGAGTCCTGGAGGCCGGTGTCCAGTGGCACCAACTAG
GTGCCCTGCTGCCCTCACAGTGGGGTTCACACCCAGGGCTCCTGGTCCCCAACACTGCC
GGCCAGGCCGTGAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGCTG
GCGACACCAGCCAGGTGCTGGTCTGGGCCAGTTCTCCCACGACGGCTCACCTCCCCCTCCAT
CTGCGTTGATGCTCAGAATGCCTACCTGTGCCCTGCGTGTAAACCACAGCCTCAGACCAGCTA
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCGGTCTGGGGTGAGGAATGTGGGAGC
TTGGGCATCCTCCAGCCTCCAGCCCCCAGGCAGTGCCTACCTGTGGTGCCAGAAA
AGTCCCCCTAGGTTGGTGGTCTACAGGAGCCTCAGCCAGGCAGCCCACCCACCCCTGGGCC
CTGCCTCACCAAGGAAATAAGACTCAAGCCATAAAAAAAA

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FIGURE 484

MRPGAPGPLWPLPWGALAWAVGFVSSMGSGNPAPGGVCWLQQQEAATCSLVLQTDVTRAEC
SGNIIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECPGKACRMLGGRPRCEAPDCS
GLPARLQVCVCGSDGATYRDECRLAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDQTGS
AHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG
GESAEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 485

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGCAGGGCCCCGGATCCCC
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTGAG**ATGAT**GGGCTTGGGA
AACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCCGCCCTGGTGGCCTGCATCATC
GTCTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGGACCTCCAGACACGGATCATG
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCGTGGAGCTGAAGAAGAAC
GAGTCCAGGGAGAGCTGGAGAAAGCAGCAGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGGCGTTTGGTGAATAACATC
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC
GGCAGGCTGCAGCAGGATGTCCTCCAGTTCAAAGAACAGACCAACCTGGAGAGGAAGTTC
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA
ATAGAAGAGGTACCAAAAAAGGGAAATGAAGCTGTAGCTTCCAGAGACCTGAGTAAAACAAAC
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCCTG
CCACACACAGAGGTGCCACAAGGGAAAGGGAAACGTGCTTGGTAACAGCAAGTCCCAGACACCA
GCCCCCAGTTCCGAAGTGGTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAACCAATGAG
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGAGCAG
GTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGAGCCGGAGAACTGGGCCAGACC
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA
GACCAGCTGTCACTCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAGGGAGAAAC
CAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA
GACAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATGTTTAAATGTTGAAGATCAG
AAAAGAGACACCATAAATTACTTGATCAGCGTGAAGAGCAGGAAATCATACACT**TGA**ATTGAA
CTGGAATCACATATTCACAACAGGGCGAAGAGATGACTATAAAATGTTCATGAGGGACTGA
ATACTGAAAATGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 486

MMGLGNRGRSMKSPPVLVAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGAV
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLHQDEKAVLVNNITTGERLIRVLQDQLKT
LQRNYGRLQQDVLQFQKNQTNLERKF SYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD
LSENNNDQRQQQLQALSEPQPRLQAA GLPHTEVPQGKGNVLGNSQTPAPSSEVVLD SKRQVEK
EETNEIQVVNEEPQRDR LPQE PGREQVVEDRPVGGRGF GGAGELGQTPQVQA ALSVSQENPEM
EGPERDQLVI PDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQA ALAGND RNI DVF
NVEDQKRDTINLLDQREKRNHTL

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 487

AAC TCAA ACT CCT CT CT GGG AAA AC GCG GT GCT GCT C CT C CG GAG T GG C CT GG C AG GG
TG TT GG AG CC CT CG GT CT G C C C G T C C G G T CT G GGG CA AGG CT GG GT T CC CT C **AT GT AT**
GG CA AG AG CT CT ACT CGT GC GG TG CT T CT C CT GG CAT AC AG CT AC AG CT CT T GG C CT
AT AG C AG CT GT GG AA ATT T A AC CT C CC GG TG CT GG AGG CT GT TA AT GG G AC AG AT G CT CG
TT AAA AT GC ACT TT CT CC AG CT T G C C C T GT GG GT AT G CT CT A AC AGT G AC CT GG A ATT TT
CG T C CT C TAG AC GGG GG AC CT GAG C AG TT GT ATT CT ACT ACC AC AT AG AT CC CT CC A ACC
AT GAG T GG G CG GT TT A AGG ACC GG TG CT T GG G AT GG G A AT C CT GAG CG GT AC G AT G C CT CC
AT C CT CT CT GG AA ACT G C AG TT G AC G A CA AT GG G AC AT AC AC CT G CC AG GT GA AGA ACC CA
C CT G AT GT T G AT GG GT G AT AGG GG AG AT CC GG CT C AG CGT CG T G C AC ACT GT AC G CT T CT
GAG AT CC ACT T C CT GG CT CT GG C AT T GG CT CT G C CT GT G C ACT G AT G AT C AT A AT AG T A ATT
GT AG T GG CT CT T CC AG C ATT ACC GG AAA AG CG AT GG CC G A A AG AG CT C AT A A AGT GG TG
GAG AT AAA AT CAA AGA AG AGG AA AGG CT CA ACC A AG A G A A A AG GT CT CT GT TT ATT TAG A A
GAC AC AG AC **TAA** CA ATT TT AG AT GG A AG CT GAG AT G ATT CC A AG A AC A AG A ACC C T AG T ATT
T CT T G A AG T TA AT GG AA ACT TT CT T GG CT TT CC AG TT GT G ACC C G T T CC A ACC AG T TC
T G C AG C AT ATT AG ATT CT AG AC A AG CA AC ACC C CT G GAG CC AG C AC AGT G CT C CT C AT AT
CA CC AGT C AT AC AC AG C CT C ATT ATT A AG GT CT T ATT A ATT C AG AGT GT AA ATT TT T CAA
GT G CT C ATT AG GT TT TATA A ACA AGA AG CT AC AT T TT G C C CT TA AG A C ACT AC TT AC AGT GT
T AT GACT T GT AT AC AC AT AT TGG T AT CAA AGGG AT AA AG CC A ATT GT CT GT TT AC T CT CT T CC
CT TT C AC GT ATT CT CT A ATT AAA AG GT GAG CT A AG C CT C CT CG GT TT CT G AT TA AC AG T AA AT C
CT AA ATT CAA ACT GT TAA AT GAC ATT TT ATT TT AT GT CT CT C CT TA ACT AT GAG AC AC AT C
TT GT TT ACT GA ATT CT T CA AT ATT CC AG GT G AT AG ATT TT GT CG

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FIGURE 488

MYGKSSTRAVLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTWT
NFRPLDGGPEQFVFYYHIDPFQPMSGRFKDRVSDGNPERYDASILLWKLQFDDNGTYTCQVK
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVLFQHYRKKRWAERAHK
VVEIKSKKEERLNQEKKVSVYLEDTD

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FIGURE 489

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FIGURE 490

MLLLWWSVVAALALAVIAPGAGEQRRRAAKAPNVVLVSDSFDRGLTFHPGSQVVKLPFINFM
KTRGTSFLNAYTNSPICCPSSRAAMWSGLFTLHTESWNNFKGLDPNYTTWMDVMERHGYRTQKF
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLRNRTKVRVMERDWQNTDKAVNWLRK
EAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIYSSDHG
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSLVDIYPTMLDIAGIPLPQNLSG
YSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD
LSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIGQNYSNVIA
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 491

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCACTGAGAGGTCTGCCATGGC
CTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACTGGT
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTATGTCGGTGCCAGCATTGTGACAGCAGT
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA
CATCTATAGCACCCCTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGAC
ATCCAGTGAATCTCCTCCCTGGCCTGCATTATCTGTGGTGGGCATGAGATGCACAGTCTT
CTGCCAGGAATCCCAGGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTACCTTGG
AGGCCTCCTGGGATTCAATTCTGTTGCCTGGAATCTCATGGGATCCTACGGACTTCACTC
ACCACTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTTTACTTGGGCATTATTC
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCCCAGAGAAATCG
CTCCAACTAACGATGCCTACCAAGCCAACCTCTGCCACAAGGAGCTCTCAAAGGCCTGG
TCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAAC
CAGGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAGCACCCGAGGGCCA
CAGGTGAGGGACACTACCACGGATCGTGTAGAAGGTGCTGCTGAGGATAGACTGACTTGG
CCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATGCAGGTTGAATTGCCAA
GGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCTCCCTGCCCTAAGTCCCC
AACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGGATCCCTTGCTGATCAA
TTACCTGGACTCCATCCCAAACCCACTAATCACATCCCAGTGAACCCCTGTGATCAA
AGACCCCTCTCTGGCTGAGGTTGGCTCTAGCTCATTGCTGGGATGGGAAGGAGAACAGT
GGCTTTGTGGGCATTGCTCAACCTACTTCTCAAGCTTCCCTCAAAGAAACTGATTGGCCC
TGGAACCTCCATCCACCTTGTATGACTCCACAGTGTCCAGACTAATTGTGCATGAAC
AAATAAAACCATCCTACGGTATCCAGGAACAGAAAGCAGGATGCAGGATGGAGGACAGGAA
GGCAGCCTGGGACATTAAAAAAATA

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FIGURE 492

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ
CDIYSTLLGLPADIQAAQAMMVTTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI
LGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQR
NRSNYYDAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

Important features:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 493

GCAC TGCT GCT GTCCC ATCAG CTGCT CTGAAG CTC **ATGGT** GCCA AGAA TCTCGCTCCTGCT
TATGTGTCAGTCTGTCTCCTCCTCTTGTCAGGAAAGTCATCGCTCCGCTGGCTCAGAA
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAGTGC
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCAATGTGGTCCCCCTGCACCTTC
TGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTTGTTGTGAAG
CTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGTGAAAGC
AGAAGACGTTTCCCT**TGAGA**AGACATAGAAAGAAAATCAACTTCACTAAGGCATCTCAGAAA
CATAGGCTAAGGTAAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTTACAAATGATGCAGCT
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA
GGAAATAAATAAAGTGGTTTCCAATGTACACACCTGTAAAAA

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FIGURE 494

MVPRIFAPAYVSVC~~LLL~~C~~P~~REVIAPAGSEPWLCPAPRCGDKIYNPLEQCCYND~~A~~IVSLSET
RQC~~G~~PPCTFWPCFELCCLDSFG~~L~~TNDVV~~V~~KLKVQGVNSQCHSSPISSKCESRRRF~~P~~

Important features:

Signal peptide:

amino acids 1-25

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FIGURE 495

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATTT
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCTGA
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTTGCT
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT
GCTTGAGCAGTGCCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG
CCCGGACCTCGGATGACAGGCTTGTGCGAGTCAGCTAATGGAACATCAGGGAACGATGA
CTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAAGAGGCTGGTGTACCTGAGATCTGGGA
TGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATTCTGTGACC
TGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAGAATTCTGGGA
CAGCATGAGATGCGTGTGCTGATGGGGCCCAGGGACTCTGAACCCCTCCTGATGACCCCTATG
GCCAACATCAACCCGGCACCCACCCCAAGGCTGGCTGGGAACCCCTCACCCCTCTGTGAGATT
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAATTATGTA
CTTTATAAATGAAAA

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FIGURE 496

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVPL
ARTQTCGNCTFRVC FEQCCPWT FMVKLINQN CDSARTS DDL RLCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 497

TGAAGGACTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTCAGCTGAAGGGAGGCACTC
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCGGC
ACAGGTGTGGCTGGTACCCGGCTGGCCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCCCTCA
GAACCAGACCAGCAGGGTAGTCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGGAGGCCAG
CGAGGGAGAAGGCCGGTGAGGAAGAGAAAGCTGGCTGATGGCCAGCAGGCAGCAGCTGCCAA
GGAGACTTCAAACCTCGGATTCAAGCCTGCGAAAGATCTCATGAGGCACGATGGCAACAT
GGTCTCTCTCCATTGGCATGTCCTGGCATGACAGGCTTGATGCTGGGGCACAGGGCC
GACTGAAACCCAGATCAAGAGAGAGGCTCCACTTGCAAGGCCCTGAAGCCACCAAGCCCAGGCT
CCTGCCCTCCCTTTAAGGGACTCAGAGAGACCCCTCCCGCAACCTGGAACGGGCCTCTC
ACAGGGAGTTTGCCTCATCCACAAGGATTTGATGTCAAAGAGACATTCTTCAATTATC
CAAGAGGTATTTGATACAGAGTGCCTGCTATGAATTTCGCAATGCTCACAGGCCAAAG
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCAAACTGTTGATGAGAT
TAATCCTGAAACCAAATTAAATTCTTGATTACATCTTGTCAAAGGGAAATGGTGCACCC
ATTTGACCCCTGTCTCACCGAAGTCGACACTTCCACCTGGACAAGTACAAGACCATTAAGGT
GCCCATGATGTACGGTGCAGGCAAGTTGCCTCCACCTTGACAAGAATTTCGTTGTCATGT
CCTCAAACCTGCCCTACCAAGGAATGCCACCATGCTGGTGGCTCATGGAGAAATGGTGA
CCACCTGCCCTGAAGACTACCTGACCACAGACTGGTGGAGACATGGCTCAGAACATGAA
AACACAGAAACATGGAAGTTTCTTCAAGTCAAGCTAGATCAGAAGTATGAGATGCATGA
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCACCCCTTGCTGACCTTAGTGAACCTCTC
AGCTACTGGAAGAAATCTCAAGTATCCAGGGTTTACGAAGAACAGTGAAGTTGATGA
AAGGGGCACTGAGGCAGTGGCAGGAATCTGTCAGAAATTACTGCTTATTCCATGCCCTCTGT
CATCAAAGTGGACCAGGCCATTCATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT
TCTGGCAGGGTGGTAATCCGACTCTCTATAATTCAAGGACATGCATAAGCAGTCGCTGCTG
TAGTAGATGCTGAATCTGAGGTATCAAACACACAGGATACCAGCAATGGATGGCAGGGGAG
AGTGGCTTTGTTCTTAACTAGTTAGGGTGTCTCAAATAAACAGTACTGCTCCCACTTA
TCTGAGGGGGATACATTCAAAGACCCCAAGCAGATGCCTGAAACGGTGGACAGTGTGTAACCT
TATATATATTTCTACACATACATACCTATGATAAAAGTTAATTATAAATTAGGCACAG
TAAGAGATTAACAATAACAACATTAAGTAAATGAGTTACTTGAACCGCAAGCACTGCAAT
ACCATAACAGTCAAACTGATTATAGAGAAGGCTACTAAGTGACTCATGGCGAGGAGCATAGA
CAGTGTGGAGACATTGGCAAGGGGAGAATTACACATCCTGGGTGGACAGAGCAGGACGATGC
AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTAGATTGTTATTCTGG
AATTTTCATTAATGTTTGGACCATGTTGACCATGGTTAAGACTGAGACTGCAGAAAGCAA
AACCATGGATAAGGGAGGACTACTACAAAGCATTAAATTGATACATATTTTAAAAAA
AAAAAA

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FIGURE 498

MKVVPSLLL SVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGEE
EKAWLMASRQQLAKETSNGFSLLRKISMHDGNMVFSPFGMSLAMTGLMLGATGPTETQIKR
GLHLQALKPTKPGPLLPSLFKGLRETL SRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYFDTE
CVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTPFDPVFTE
VDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDH LALEDY
LT TDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI FSPFADLSELSATGRNLQ
VSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLFLGRVVNP
TLL

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FIGURE 499

CTAGCCTGCGCCAAGGGTAGTGAGACCGCGCGAACAGCTTGC GGCTGC GGGGAGCTCCG
TGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATGG**ATT CTTGC GGAAAATGCTGATCTCAGTCG
CAATGCTGGCGCAGGGCTGGCGTGGCTACGCGCTCCTCGTTATCGTACCCCCGGAGAGC
GGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAGGCCG
CCAGGACCCAGCAGCTATTGCTGGCACTCTGCAGGAGGCAGCGACCACGCAGGAGAACGTGG
CCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGCGGCCAGCGGGAGGTACCG**TGA**GACC
GGACTTGCCTCCGTGGCGCCGGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCCTTCTCC
TTCGTGGGCCAGCGGAGAGTCGGACCGAGATAACCATGCCAGGACTCTCCGGGTCTGTGA
GCTGCCGTGGGTGAGCACGTTCCCCAAACCCCTGGACTGACTGCTTAAGGTCCGCAAGGC
GGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAATCATGTT CCT
CCAAAAAAA

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FIGURE 500

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLAT
LQEAAATTQENVAWRKNWMVGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 501

CAGGAGAGAAGGCACCGCCCCACCCGCCTCCAAAGCTAACCTCGGGTTGAGGGGAAGAG
GCTGACTGTACGTTCTTCTACTCTGGCACCACTCTCCAGGCTGCCATGGGCCAGCACCC
TCTCCTCATCTTGTTCCTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCTGT
GGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACCAGAG
TAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAAGATGCTGCCACTGCTGGAGGTGGC
AGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCACACCATCTCCGGGAGAGTGGATCGTCT
GGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGTTGATGA
GAAGGTGACTGGAGGCCCTGGGACCAAAGGAAGAAGGAATGAGAAAGTACGATATGGT
GACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCGATTGGTGG
CCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACGTGTTAGATGG
GACACAGAAATGACACAGCCTTGTCTCCAAAGGCTGCGTACTTCACCCCTGCCATGGCTGC
CCGGAAAGCTCCCGAGTCCGGGTGCCCTCCCCCTGGTAGGCACAGGGCAGCTGGTATATGG
TGGCTTCTTATTTGCTCGGAGGCCTCTGGAAAGACCTGGTGGAGGTGGTGGAGATGGAGAA
CACTTGCAAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGACAGCTCAGTATTCCC
AGCAGAGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACATGACCTGGTAGCTGA
TGAGGAAGGTCTTGGCTGTCTATGCCACCCGGGAGGATGACAGGCACCTGTGTCTGGCAA
GTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCCTGCTCCAGAGAGAATGC
TGAGGCTGCCTTGTCTATGTGGGACCCCTATGTCGTCTATAACACCCGCTGCCAGTCG
GGCCCGCATCCAGTGCTCTTGATGCCAGCGCACCCCTGACCCCTGAACGGCAGCACTCCC
TTATTTCCCCGCAAGATATGGTCCCCATGCCAGCCTCCGCTATAACCCCCGAGAACGCCAGCT
CTATGCCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGAGATGAGGAAGAAAGAGGAGGA
GGTTTGAGGAGCTAGCCTGTTTGCATCTTCACTCCCACATTTATATTATCCC
CACTAAATTCTTGTTCCTCATTCTCAAATGTGGGCCAGTTGTGGCTCAAATCCTCTATATT
TTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTTCATACGGAACCTCCAGATCCTGAG
TAATCCTTTAGAGCCGAAGAGTCAAAACCCCTCAATGTTCCCTCCTGCTCTGCCCATG
TCAACAAATTCAAGGCTAAGGATGCCAGACCCAGGGCTTAACCTGTATGCCAGGCC
CAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTGACTTGGGGAGGGAGAAATAGGAGGAGA
CGTCCAGCTGTGCTCTTCCCTCACTCCCTTCAGTGTGCTGAGGAACAGGACTTCTC
CACATTGTTGTATTGCAACATTTGCATTAAAAGGAAATCCACAAAAAAAAAAAAAAA
AAA

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FIGURE 502

MGPSTPLLILFLLSGPLQGQQHHLVEYMERRLAALEERLAQCQDQSSRHAELRDFKNKML
PLLEVAEKEREALRTEADTISGRVDRLEREV DYLETQNPALPCVFDEKVTGGPGTKGKGRNN
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF
TLAMAARKASRVRPFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFH LANRTVV
DSSVFP AEGLIP PYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQQWDTP
CPRENAEA AFVIC GTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFP RRYGAHASLRYN
PREROLYAWDDGYQIVYKLEM RKKEEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 503

TGC GGCG CAGT GTAG ACCT GGGAGG **AT**GGC GGC CTG CTG CTG CTG CTT TCT GG CTT GGT
CTC GGT GCC CAGG GCC CAGG CGT GTGG TT GGG AAG ACT GG ACC CTG AGC AGC TT GGG CC
CTGGTACGTGCTTGC GG TGCC CCCC GGG AAAAGGG CTTGCC ATGG AGA AGG ACATGA AGAA
CGT CGT GGGGGT GGT GGT GAC CCT CACT CCAG AAAACA ACCT GCG GAC GCT GT CCT CTCAGCA
CGGG CTGG AGGG GT GTG ACC AG GT GT CATGG ACCT GATA AAC CGAA ACT CCGG ATGG GT TT
TGAGA ATCC CT CAATAGG CGT GCT GGAG CT CTGG GT GCT GGG CACCA ACT TCAG AGA CT AT GC
CATCAT CTT CACT CAG CT GGAG T C GGGG AC GAG CC CTT CAAC ACC GT GGAG CT GT AC AGT CT
GACGGAGACAGCCAGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGCCTGGCTT
CCTGTCACAG **TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGATCCTCTGTG
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCAGTGTCCACCC
ACCTCGCTCAGCGGCTCCGGGGCCAGCACCACTCAGAATAAGCGATTCCACAGCA

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FIGURE 504

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVTL
TPENNLRITLSSQHGLGGCDQSVMVDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQLEF
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20

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FIGURE 505

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC
CTGCTTGCTCTGGCAACAGGGTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAGTGC
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGGGGCG
ACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACATAGTT
CACCTGGGGCAGCACAAACCTCCAGAAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG
TCCTCCCCCACCCGGCTTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG
CTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCCCTCTCCTCA
CGCTGTGTCAGTGCCTGGCACCAGCTGCCTCATTCCGGCTGGGCAGCACGTCCAGCCCCAG
TTACGCCTGCCTCACACCTTGCATGCACATCACCATCATTGAGCACCAGAAAGTGTGAG
AACGCCCTACCCGGCAACATCACAGACACCATTGGTGTGCGCAGCGTGCAGGAAGGGGCAAG
GACTCCTGCCAGGGTACTCCGGGCCCTCTGGTGTGTAACCAGTCTTCAAGGCATTATC
TCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTGTACACGAAAGTCTGCAA
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATAGACTGGACCCACCCACAGCCCA
TCACCCCTCCATTCCACTTGGTGTGTTGGTCTGTTCACTCTGTTAATAAGAAACCTAAGCC
AAGACCCCTACGAACATTCTTGGCCTCTGGACTACAGGAGATGCTGTCACTTAATAATC
AACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTGAAATATTGTGACTCTG
GGAATGACAACACCTGGTTGTTCTGTGTTGATCCCCAGCCCCAAAGACAGCTCCTGGCCAT
ATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 506

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAC
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV
RPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTMVCA
SVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAIRKPGVYTKVCKYVDWIQETMKNN

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 507

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTACAGAGACGCGGACCCCAGACATGAGG
AGGCTCCTCCTGGTACCCAGCCTGGTGGTTGTGCTGTGGGAGGCAGGTGCAGTCCCAGCA
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGCCCTCAGAGCAGGACCCAGAGAAGGCC
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC
CAGAACGCCAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAAGGCAGGGGCCCCATCCTT
CCAGGCACCAAGGCCTGGATGGAGACCGAGGAACCCCTGGCCGTGTCCCTGAGTCCCAGGCC
GACCATGACAGCCTGTACCAACCCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCGGGTG
TGGGTGATGCCAAATCACCAGGTGCTCCTGGACCGGAGGAAGACCAAGACCACATCTACCAC
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCTGTCCCAAGGCCAGGCTGTTGGGA
CTGGGACCCCTCCCTACCCCTGCCAGCTAGACAAATAACCCAGCAGGCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 508

MRRLLLVTSLVVVLLWEAGAVPAPKVKPIKMQVKHWPSEQDPEKA
VGARVVEPPEKDDQLVVLF
PVQKPPLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSL
YHPPPEEDQGEERP
RLWVMPNHQVLLGPEEDQDH^IYHPQ

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FIGURE 509

GC GGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCGCCGCCACCTCGGCTGGGAGCCC
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGAGGTGCTGGGCCGCG
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCATGAAAGCGCAGCCATG
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACACTCCAGTGCTAACTAACAGAG
ACTCTCCAACATGTGCCTCTGACCATAACAAATGAAACACTCCAACAGTACTGTGAAACCACCA
ACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT
AATACAACAAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTAAAGTCTACACCC
AAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCATTCTGAAGCA
AAGAAAGGATCAAAATTGATACTGGAGCTTGTGGTATTGTATTAACGCTGGAGTT
TTATCTATTCTTACATTGGATGCAAAATGTATTACTCAAGAACAGGCATTGGTATCGAAC
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT
GCTGCCCTATCAATTAAATTGGTTATTAAATAGTTAAAACAATATTCTTTTGAAATA
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGAAAGATTCTCAAGG
TAACAAGGGTTGGGTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTT
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTGGCTGGGTGGGCATTGG
TCACATATGACCAAGTAATTGAAAGACGTCACTGAAAGACAGAATGCCATCTGGGCATACA
AATAAGAAGTTGTCACAGCACTCAGGATTTGGTATCTTAGCTCACATAAGAAACTT
CAGTGCTTTCAAGAGCTGGATATCTTAATTACTAACAGAACAGAAATTATAACATCAAA
CTAGATCTGAAGCATAATTAAAGAAAAACATCAACATTTTGCTTAAACTGTAGTAGTT
GGCTAGAAACAAAATACTCC

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FIGURE 510

MGLGARGAWAALLLGTIQLVIALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDHT
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTPGMVSTNMTSTTLKSTPKTTSVSQNTS
QISTSTMVTNHNSVTSAASSVTITTMHSEAKGSKFDTGSFVGGIVLTLGVLSILYIGCKM
YYSSRRGIRYRTIDEHDAAII

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FIGURE 511

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FIGURE 512

MARMSFVIAACQLVLGLLMTSLTESSIQNSECPLCVCEIRPWFTPQSTYREATTVDCNDLRL
TRIPSNLSSDTQVLLQSNNIAKTVDELQQLFNLTELDFSQNNFTNIKEVGLANLTQLTTLHL
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNNLLHLNSNKLKVIDSRWFDS
TPNLEILMIGENPVIGILDMMNFKPLANLRSVLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV
KVPQLALQKVPNLKFLLDKNPKIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLP
KLEATNNPKLSYIHRLAFRSVPALESMLNNNALNAYQKTVESLPNLREISIHSNPLRCDCV
IHWINSNKTNIRFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNV
QGADTRVATIKVNGETLQDGTVQLKIYVKQTESHSILVSWKVNSNVMTSNLKSSATMKIDNPH
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAAFAVDISDQETST
ALAAVMGSMFAVISLASIAIVYFAKRFKRKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE
DKDGSAADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73; 96-100; 106-110; 117-121; 385-389; 517-521;
582-586; 611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22; 224-230; 464-470; 637-643; 698-704

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FIGURE 513

GGGAGAGAGGATAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTCC
CAGCAATATGCATCTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGCCCT
GTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTCCAATCACGCATGC
CGGAAGGAAAGTGGAGAAGGTTCAACGGACTTAGCAACATGGGAGCCACACCGGCAAGGA
GTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAAACTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACCAAGGCCGTTAGCCTCTGGGCCTCAGTCAA
CGGATCTTCCAGCCATCAAGGAGGGCCACAAACCACGCCGTTAGCCTCTGGGCCTCAGTCAA
CACGCCTTCATCAACCTCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 514

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP

Important features:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 515

CCACCGTCCGCCACCGTCCGGTGCACACTCGCGCCGGCGCCTCCGGCTTCTCTT
TTCCCTCGACCGGCCACGGCTGCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCGAA
CCCCCTCGCGGAGAGGAGCGAGGCAGGGTGGCCCCGGGCGCGTTGGTCTCGGAG
AAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCCGACTGACGCGAGTTGGGG
CCCGACTACCGCAGCTGACAGCGCATGAGCGACTCCCCAGAGACGCCCTAGCCCCTGTG
CGGCCAGGCGAGCGCGCAGGTGGGCTGGTAGTGGTCCGCCACGCCGGTCGCCG
GCCGCCAGGATGGCGCTGGCAACCCGGGCCGCCGCTGCTACCCCTGCGCCCGC
TGCAGGCCGGTCCGGCCGCCCCGCTCATGGACGGCGCTCCGGCTGGCGCGGC
GCGCCCCGGCTGTGAATGCGACTGCCCTCGCCGCGCTCCCGCCGCCGCCGG
GACGTGGTAGGGATGCCCAGCTCCACTCGATGGCAGTTGGCGCCTCCAGTTCCCTCCT
GGTCACCTGCTGCCCTGATGGTGGCTCTGTGCACTGGCAGCATTCCGCTGGAGAACGCTGGCCA
GGCACCAAGAGCAGCCGGCCAGGAGAACGCGAGCACGCCACTCGGACGCCGGGG
GAACGAGCTCGGGGCCCGCGAGGGACGAGGGCGCAGCGGCCGGACTGGAAGAGCAAGAG
CGGCCGTGGCTGCCCGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCCTGGCTCCAGGG
CGGGGGCGCAAGGCCGGGATCTGCAGGTCCGGCCCGCGGGACACCCGCAGGCCAG
CCTGGCCGAGCCGCCAGGACGCATTGGCCCGAACCGGCCACGCCGAGCCACCGA
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGAGAGCGGCTCGTGTACGC
GATCGGGGAGAAGTTCGGCCGGCCCTCGGCTGCCGTGCGCTGTGACCGAGGGGCC
GCTGTGCCGCAGCCCGAGTGGCCGAGGCTGCACCCGCGCTGCATCCACGTGACACGCCA
GTGCTGCCGCAGTGCAAGGAGAGGAAGAAACTACTGCGAGTTCCGGGCAAGACCTATCAGAC
TTTGGAGGAGTCTGGTGTCTCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT
ATGCACAGTGTCAAGCGTGTCCCCAGACGGAGTGTGTGGACCCGTGTACGAGCCTGATCAGTG
CTGTCATCTGAAAAATGGTCAAACGCTTGCAGAAACCGCGGTGATCCCTGCTGGCAG
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT
CGAGCGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGCGCTCCAGAACACA
AACTCTGACTTTCTAGAACATTACTGATGTGAACATTCTAGATGACTCTGGAACTATC
AGTCAAAGAAGACTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTCTTGTATA
ACAGTTACTACAACAGAAGGAAATGGATATTTCAAACATCAACAAGAACTTGGGCATAA
AATCCTCTCTAAATAATGTGCTATTCACAGTAAGTACACAAAGTACACTATTATAT
CAAATGTATTCATAATCCCTCATTAGAGAGCTTATATAAGTGTCTATAGATGCAGAT
TAAAAATGCTGTGTCAACCGTAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 516

MPSSTAMAVGALSSSLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRREHATRDGPGRVNELG
RPARDEGGSGRDWKSKGRLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALAAA
AQDAIGPELAPTPEPPEYVYPDYRGKGCVDESGFVYAIKEKFAPGPSACPCLCTEEGPLCAQ
PECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVLCTVS
ACPQTECVDPVYEPDQCCPICKNGPNCFAAETAVIPAGREVKTDECTICHCTYEEGTWRIERQA
MCTRHECRQM

Important features:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

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FIGURE 517

GGACAACC GTT GCT GGG GTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC
GGACGACGCCTATGAAGGCCCTAGTCCTCTAGTTGCGCTTTGCTATGGCCTCGTCTGTGC
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTGAAATCATTATACAG
TTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAAATCTAATC
CTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAGGAGCTAGTTACACATG
GAGACGCTTCAACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAAATACAACATTCC
CTACAGGAGGCTTACACCGAAATAGGAAAGAAAAACACACGGAAAGTACCCATTCTGGT
CGATCAAACCAAACATGTTCCATTGTTGCATGCAGAGAACCTTATATTGAAAATGAAG
AGCCAGAGCCAGAGCCGGAGCCAGCTGAAAACAAACTGAGGCACCAAGAATGTTGCCAGTTG
TTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCACTTACAG
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAAACTG
CGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAATGATGACATTTGA
AAAAAATTTAGATATTAATTCAAGTGCAACAGGCACCTCTTAGTGCACACCAGCAACCCAG
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCCTGCTTAGCAGCAG
CAGCAGAACATAAAATAAAAAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA
ATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATTCTAGATCTAAACTCTATG
AATATTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA
CATTAATGAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTATTAAACAATAA
TATAAAAATTTAACCTACTGATATTCCATAACAAAGCTGATTAAAGCAAACTGCATTTT
TCACAGGAGAAATAATCATATTGTAATTCAAAGTTGATAAAAATTTCTATTGAGT
TCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACAATTTCATATGCACTAAAACC
TAATTAAAATAAAATTTGGTTCAGGAAAAAA

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FIGURE 518

MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKNSPKH
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKTESTPFWSIKP
NNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTLKDSTG
IEISTESEDVPQLSGETAIEKPEEFGKHPEWNNDDILKKILDINSVQQALLSDTSNPAYRE
DIEASKDHLKRSLALAAAEEHKLKTMYSQQLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 519

CGGCTCGAGTGCAGCTGTGGGGAGATTCAGTCATTGCCTCCCTGGGTGCTTCACTCTTG
GATTGAAAGTTGAGAGCAGC**ATG**TTTGCCCCACTGAAACTCATCCTGCTGCCAGTGTACTG
GATTATTCCCTGGGCCTGAATGACTTGAATGTTCCCCGCTGAGCTAACAGTCATGTGGGT
GATTCACTCTGATGGGATGTGTTCCAGAGCACAGAACAAATGTATATTCAAGATAGAC
TGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC
AGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTGATGGGGACATCTTATGCAATGAT
GGCTCTCCTGCTCCAAGATGTGCAAGAGGGCTGACCAGGGAACCTATATCTGTGAAATCCGC
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGGCGGTGGTACTGCATGTGCTCCAGAGGAGCCC
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAAGATGGATGTGTTCCAGAGCACAGAA
GTGAAACACGTGACCAAGGTAGAATGGATATTCAGGACGGCGCGAAAGGAGGAGATTGTA
TTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGCCACTCCAG
AATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATGCTTCAAGGAGTG
AGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGAAACCTGGTGTCAAGAAA
ACCATTGTGCTGCATGTCAAGCCCGAAGAGCCTCGAACACTGGTGACCCGGCAGCCCTGAGG
CCTCTGGTCTGGTGGTAATCAGTTGGTGTACATTGTGGAATTGTCTGTGCCACAATCTG
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTGAATTCT
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCTGCCATTT
GAAAGATGTGAAGGGGAGAAACACATTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA
GAAGAACCAAGTGAAGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGTCACTCGAACACTCACTGAAAAAAAGTCAGGTGGGGAAATGCCAAAAACACAGCAA
GCCTT**TG**AGAAGAATGGAGAGTCCTCATCT**CAGCAGCGTGGAGACTCTCTGTGT**
GTCCTGGGCCACTCTACCACTGATTTCAGACTCCGCTCTCCAGCTGTCTCCTGTCTCATT
GTTTGGTCAATAACTGAAGATGGAGAATTGGAGCCTGGCAGAGAGACTGGACAGCTGTGGA
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGACACTGGCCCTG
GGAACCCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACCCTCCTGTGGCAGGG
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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FIGURE 520

MFCPLKLILLPVLLDYSLGLNDLNVPPELTvhVGDSALMGCVFQSTEDKCIFKIDWTLS PGE
HAKDEYVLYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV
FKKAVVLHVLPEEPKELMVHGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL
RMSVEYSQSWSGHFQNRVNLVGDIFRNDGSIMLQGVRESDGNNYTCSIHLGNLVFKKTIVLHVS
PEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLI LIVKKTCGNKSSVNSTVLVKNT
KKTNP EIKEKPCHFERCEGEKHISPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNNS
LEKKSGGGMPKTQQAF

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FIGURE 521

CTATGAAGAAGCTCCTGGAAAACAATAAGCAAAGGAAACAAATGTGTCCCATCTCACATGG
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA
ACTACATTTGCAAAGTCATTGAACCTGAGCTCAGTTGCAGTACTCGGGAAAGCC**ATGC**CAGGA
TGAAGATGGATACATCACCTTAAATATTAAAACCTGGAAACCAGCTCTCGTCTCCGTTGGCCC
TGCATCCTCCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGTGCGTGGGGATGGT
TGTGGGGCTGGTGGCTCTGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGATGAGAA
TGAAAATCGCACAGGAACCTGCAACAAATTAGCAAAGCGCTCTGTCAATATGTGGTAAAACA
ATCAGAACTAAAGGGCACTTCAAAGGTATAAATGCAGCCCTGTGACACAAACTGGAGATA
TTATGGAGATAGCTGCTATGGGTTCTCAGGCACAACCTAACATGGGAAGAGAGTAAGCAGTA
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA
AGCCAGGACTATTAAATCGTGGCTGGATTATCTGCCAGAAGTCGAATGAGGTCTGGAA
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTTGGAAAGATGGAAAAGGAAA
TATGAATTGTGCTTATTTCATATAATGGAAAATGCACCCCTACCTTCTGTGAGAACAAACATTA
TTAATGTGTGAGAGGAAGGGCTGGCATGACCAAGGTGGACCAACTACCT**TAA**TGCAAAGAGGT
GGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA
GCTGAAAAAAAAAAAAAA

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FIGURE 522

MQDEDGYITLNKTRKPALSVGPASSSWRVMALILLILCVGMVVGVALGIWSVMQRNYLQ
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEEES
KQYCTDMNATLLKIDNRNIVEYIKARTHЛИRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG
KGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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FIGURE 523

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGC
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCCAA
GAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGCCCTA~~ACT~~CTAAT
TGTCTGTTGGGGAGCAAGCACTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA
GCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAAG
AACTGAAATATTCAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTAAAAA
CGGATACACTGGCATCTACTCGTGGTCTCBBBBBAGTAAACTCAGATTAAAGT
GATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCAACTTT
CTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTCTTAA
AAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATCCACTCTAAT
ATCAGTTCTGAGTTACAAGACTTGAGGAGGAGGAGAAGATCTTCACTTCTGCCAACGA
AAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCG
TCACGCCAGACAAGCAAGTGGAGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA
ATTTGATCCCAGTCGATGAGAGAGGTTATTGTTGATTACTGCCGTCGAGGCAACCGCTA
TTGCCGCCGCGTCTGTGAACCTTACTAGGCTACTACCCATATCCACTGCTACCAAGGAGG
ACGAGTCATCTGCGTGTCACTGCCTTGTAACTGGTGGTGGGCCGCATGCTGGGAGGGT
CTAATTAGGAGGTTGAGCTAAATGCTTAAACTGCTGGCAACATATAAAATGCATGCTATT
CAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTGTAG
GTAATTCTCTTCAATTACATTACACCAAAAAAAAAAAAAAA

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FIGURE 524

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYD
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI
KVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT
LISVSELQDFEEEEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG
IEFDPMLERGYCCYCRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
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N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

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FIGURE 525

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATGAAGATCACTGGGGTC**
TCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCACAT
ACCTACCAGTTGTGGTCTGACTACATCACCTATGGAATGAATGTCAGTTGTGTACCGAGA
GCTTGAAGAAGTAATGGAAGAGTTCAGTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCATGGAC
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTCATCCCAGGCTCTGACTGAGTTTC
TTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGGCCAGATTCAAGAGTAATCTGACTGAAT
GGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTT
TAACACGTCAATAAAAAATAATCTCCCAGA

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FIGURE 526

MKITGGLLLLCTVYYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE
CHLCTESLKSNDRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 527

CGACG**ATG**CTACGCGGCCGGCTGCCTCCTCCGGACCTCCGTAGCGCTGCCGCCCTGG
CTGCGGCCGCTGCTCTCGCTTGCGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGCCT
CGTCGCTCAGCCCCATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCATTGT
CGGGCCCCGAGGCTCCGTGGCGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGTGCAGC
TGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGAAGCTGAGGC
AGCTGCACGGGTTGCTGCAGGCCGCGGGTCCAGGGATGGCGGGCTAGTAGTACCGGCAGCC
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTGTGGTACGCGGACTGGATGGACGGGCAGC
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCCTCGCTTCCC
CCCTTTCAAGCGTGAAGAACTACGGCCGCTGCCTCGTACACCAGTTCCAAGCACCGCTGCA
TGGATAGCAGCGCCGCCCTCCTGCAGGGCTGTGGCAGCACTACCACCCGGCTGCCGCC
CGGACGTCGAGATAATGGAGTTGGACCTCAACAGTTAATGATAAAACTAATGAGATTTTG
ATCACTGTGAGAAGTTTAACTGAAGTAGAAAAAAATGCTACAGCTTTATCAGTGGAAAG
CCTTCAAAATGGACCAAGAAATGCGAGAACATTAAAAAAAGTTGCAGCTACTTGCAAGTGC
CAGTAAATGATTAAATGAGATTAACTCAAGTAGCCTTTCACCTGTTCATTTGACCTGG
CAATTAAAGGTGTTAAATCTCCTGGTGTGATGTTTGACATAGATGATGCAAAGGTATTAG
AATATTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTATACTATTACAGTCGAT
CCAGCTGCACCTGTTCAAGGATATCTTCAGCACTGGACAAAGCAGTTGAACAGAAACAAA
GGTCTCAGCCAATTCTCCAGTCATCCTCCAGTTGGTCATGCAGAGACTCTTCTCCAC
TGCTTCTCTCATGGGCTACTTCAGAACAGAACCCCTAACAGCGTACAATTACAAAAAAC
AAATGCATCGGAAGTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTGTC
TTTACCACTGTGAAAATGCTAAGACTCTAAAGAACAAATTCCGAGTGCAGATGTATTAAATG
AAAAGGTGTTACCTTGGCTTACTCACAAGAAACTGTTCATTTATGAAGATCTGAAGAAC
ACTACAAGGACATCCTTCAGAGTGTCAAACCAAGTGAAGAATGTGAATTAGCAAGGGCTAAC
GTACATCTGATGAACTAT**G**TAACTGAAGAACATTAAATTCTTAGGAATCTGCAATGAG
TGATTACATGCTGTAATAGGTAGGCAATTCTGATTACAGGAAGCTTTATATTACTGAG
TATTCTGTTTCAACAGAAAACATTGGGTTCTCTCTGGGTTGGACATGAAATGTAAGA
AAAGATTTTCACTGGAGCAGCTCTTAAGGAGAAACAAATCTATTAGAGAAACAGCTGGC
CCTGCAAATGTTACAGAAATGAAATTCTCCTACTTATAAGAAATCTCACACTGAGATAG
AATTGTGATTCTATAAAACACTTGAAAAGTGTGGAGTAACAAAATATCTCAGTTGGACCAT
CCTTAACCTGATTGAACTGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTTTCC
TCAGGTAGGACAGCTCTAGCATTCTTAATCAGGAATTGTGGTAAGCTGGAGTACT
CTGGAAAGAAAGTAACATCTCCAGATGAGAATTGAAACAAGAAACAGAGTGTAAAAGGAC
ACCTTCACTGAAGCAAGTCGGAAGTACAATGAAAATAAATATTGGTATTATGAA
ATATTGAAACATTTCATAAAATTCTTACTTCTAGGAAGTCTCAAAGACCATTAA
ATTATTATATGTTGGACAATTAGCAACAAGTCAGATAGTTAGAATGAAAGTTCTCAAATCC
ATTGCTTAGCTAACTTTCTATTCTGCACTGGCTTCGATTTTATATTCTTCTATTATGAA
AAATGTATCTTGGTTGTTGATTCTTCTTCTTGTAAATAGTTCTGAGTTCTGTCA
AATGCCGTGAAAGTATTGCTATAAAAGAAAATTCTGTGACTTAAAAAA

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FIGURE 528

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLSG
PEAPWRDPELLEGTCVPQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGSSTGSRD
LGAALADWPLWYADWMQQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF
KTGPEMQNILKKVAATLQPVVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDAKVLEY
LN DLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVLQFGHAETLLPLL
SLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRVQMLLNEK
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 529

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTGG
CGGAGAGATCAGAACGCTCTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGGA
CGCGCGCGCGCGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGGCCGGGGCG
GTGATTGCAGCCCCAGACAGCGCGCTGGCTGTGGTCGGCTGGCGGCCGCTGGGCTC
TTGACAGCTGGAGTATCAGCCTGGAAGTATATAACGCCAAAGAAATCTCGTGGCAAATGGT
ACACAAGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC
TCCTGGAGCTCCAGCCAGAGGGGGCGACACTACTGTGCTTTCCACTACTCCAAAGGG
CAAGTGTACCTGGGAATTATCACCATTAAAGACAGAATCAGCTGGCTGGAGACCTTGAC
AAGAAAGATGCATCAATCAACATAGAAAATATGAGTTATACACAATGGCACCTATATCTGT
GATGTCAAAACCTCCTGACATCGTTGCTCAGCCTGGACACATTAGGCTCTATGTCGTAGAA
AAAGAGAATTGCGCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTGCTGTGGCTTA
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGCTCTATAGAAGGAAAACCTAAACGG
GATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACGAGGCTCCCGAAGTCC
CCCTCCGACACTGAGGGTCTTGTAAAGAGCTGCCTCTGGATCTCACAGGGCCCAGTCATA
TATGCACAGTTAGACCACTCCGGCGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG
GTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA
ACCAAACGGACTCTCGTGCAGAAAATGTAGCCCATTACACATGTAGCCTGGAGACCCAGG
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAAGATGTGTACAAAGGATATGTATAAA
TATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGATGATGAAAAGATGGTATGATTC
TACATATGTACCCATTGTCTGCTTTGTACTTTCTTCAGGTCAATTACAATTGGGAG
ATTCAGAAACATTCCCTTACCATCATTAGAAATGGTTGCCTTAATGGAGACAATAGCAG
ATCCTGTAGTATTCAGTAGACATGGCCTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATAACCAGGGTGGCCTTAGC
ACAGTATCAGTACCAATTATTGTCTGCCGCTTTAAAAAATACCCATTGGCTATGCCACTTG
AAAACAATTGAGAAGTTTTGAAGTTCTCACTAAAATATGGGCAATTGTTAGCCTT
ACATGTTGTAGACTACTTAAGTTGCACCCCTGAAATGTGTCAATATCAATTCTGGATT
CATAAAGATTAGCAAAGGATAATGCCAAGGTCACTCATTCTGGACACAGTTGGAT
CAAACTGATTAAGTAGAAAATCCAAGCTTGCTTGAGAACTTTGTAACGTGGAGAGTAAA
AGTATCGGTTTA

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FIGURE 530

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPFKDRISWAGDLDKKDASINENMQ
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLLISMILAV
LYRKRNSKRDYTGCSTSESLSVKQAPRKSPSDTEGLVKSLSHQQGPVIYAQLDHSGGHHS
DKINKSESVVYADIRKN

Important features:

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 531

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCGA
GGCTGGTGGAAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC
TTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGCTGCCGGCCGGACTGGT
GCGCGAGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTCACGGTGGGCTGCTGCTG.
GAGCACTCATTGAGATCGATGACAGTGCACACTCCGGAAGCAGGGCTCACTGCTCTGGAAC
CAGCAGGATGGTACCTTGTCCCTGTCACAGCGCAGCTCAGCGAGGAGGAGCAGGGCCGACTC
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAGGCGACCCGGGGCCCTG
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGGTGGAGTCG
CACCTGTCGGACCAGCTGACCTGCACGTGGATGTGGCCGGCAACGTGGTGGCGTGTGGTG
GTGACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG
CGCCTGGAGATGGAACAGGCCAGAAGGCAAGAACCCCCAGGAGCAGAAGTCCTTCTCGCC
AAATACTGGATGTACATCATTCCGTCGTCCTGTTCTCATGATGTCAGGAGGCCAGACACC
GGGGGCCAGGGTGGGGTGGGGTGGTGGTGGGGTAGTGGCCTTGCTGTGCCA
CCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTGAAATGTGTGAAACGTTTGAAAA
GCTACAGCTTCCAGCAGCAAAGCAACTGTTGTTGGCAAGACGGCCTGATGTACAAGCT
TGATTGAAATTCACTGCTCACTTGATACGTTATTCAAGAAACCCAAGGAATGGCTGTCCCCATC
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGGCAGTTATTAAACTGTCCCCAGATC
GACACGCAAAAAAAA

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FIGURE 532

MAAASAGATRLLLLLMAVAAPSRARGSGCRA GTGARGAGAEGREGEACGTVG LLLEHSFEID
DSANFRKRG SLLWNQQDGTLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPGALDGLEAGG
YVSSFVPACSLVESHLS DQLTLHVDVAGNVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP
PTTAPGPETAAFIERLEMEQAQKAKNPQE QKSFFAKYW MYIIIPVVLFLMM MSGAPDTGGQGGGG
GGGGGGGSGLCCVPPSL

Important features:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 533

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGCTGGTGGTGA
GGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGAC
TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGG
CCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAA
GACCCAGGGTGC GG CATCTACAAGGACAACAACAAAGCAGCATA CATTGTATGGATTATC
TCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTCCGAATA
AAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 534

MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC
CQTHDCCYDHHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFVNVIYLENEDSE

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

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FIGURE 535

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCTG
AACTGGGTGCTCATCACGGGAACGTGCTGGCTATGAAATACAGATGTGGCAGCTCAGGTAGCC
CCAAATTGCCCTGGAAGAATAACATCATGTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTT
TTTTAACCGCCCCCTCCCACCCCCCAAAAAACTGTAAAGATGCAAAACGTAATATCCAT
GAAGATCCTATTACCTAGGAAGATTGATGTTGCTGCGAATGCGGTGTTGGGATTTATTT
GTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCAAATCGGTCCATCTCCAAAG
GGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTCAGCTGACAGGGG
CTGTCATGCAACTGGCCCTAAGCCAAAGCACCTAAGGACGACCTTGAAACAATACAA
AGG**ATGGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTAGCCCCC**
ACTGTCTTACTGACAATGCTTCTGCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTAAGTATCTGCTGGT
TGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAATCAATTAAAGGG
CTCAACCAGCTCACCTGGCTACCTGACCATAACCATAACGAAATTGACGAAAATGCT
TTAATGGAATACGCAGACTCAAAGAGCTGATTCTAGTTCCAATAGAATCTCCTATTTCCTT
AACAAATACCTCAGACCTGTGACAATTACGGAACCTGGATCTGCTCTATAATCAGCTGCAT
TCTCTGGGATCTGAACAGTTGGGGCTTGCAGGACTGCTGAGTTACATTACGGTCTAAC
TCCCTGAGAACCATCCCTGTGCGAATATTCAAAGACTGCCGAAACCTGGAACCTTGGACCTG
GGATATAACCGGATCCGAAGTTAGCCAGGAATGCTTGCTGGCATGATCAGACTCAAAGAA
CTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCTTTTCCAAGGTTGGTCAGC
CTTCAGAACCTTACTTGCAGTGGAAATAAAATCAGTGTCTAGGACAGACCATGCTGGACC
TGGAGCTCCTACAAAGGCTTGATTATCAGGCAATGAGATCGAAGCTTCACTGGACCCAGT
GTTTCCAGTGTGTCCCAGCTGAGCTGGCTTGCAGCAGCCTCAACCTGGATTCCAACAAGCTCACATTATT
GGTCAAGAGATTGGATTCTTGATATCCCTCAATGACATCAGTCTGCTGGGAATATATGG
GAATGCAGCAGAAATATTGCTCCCTGTAAACTGGCTGAAAGTTAAAGGTCTAAGGGAG
AATACAATTACTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTGATCTGGCCAGGGCTCTCCCAAAG
CCGACGTTAACGCCAAGCTCCCCAGGCCAGCATGAGAGCAACCCCTTGCCCCCGACG
GTGGGAGCCACAGAGCCCCGGCCAGAGACCGATGCTGACGCCAGCACATCTCTTCCATAAA
ATCATCGGGGCAGCGTGGCGTTTCTGTCCGTGCTCATCCTGCTGGTTATCTACGTG
TCATGGAAGCGGTACCCCTGCGAGCATGAAGCAGCTGCAAGCAGCCTCATGCGAAGGCAC
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTATGTAGAT
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTAT
AACAAATGGGCTCCAGGGAGTGTGAGGTAT**TGA**ACCATTGTGATAAAAAGAGCTTAAAGC
TGGGAAATAAGTGGTGTCTTATTGAACTCTGGTACTATCAAGGAAACCGCATGCCCTTCTC
CCCTCCCTCTCCCTCACTTGGTGGCAAGATCCTCCTGTCCGTTAGTGCATTCTA
ATACTGGTCATTTCTCATACATAATCAACCCATTGAAATTAAATACCACAATCAATGT
GAAGCTGAACTCCGGTTAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAAAT
GTCGCATTGTTAAGATAAAACTTCTTCATAGGTAaaaaaaaaaaaaaa

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FIGURE 536

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCGKMYCSEQKLQEIPSSISAGC
LGSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIIDENAFNGIRRLKELILSSNRISYFLN
NTFRPTVNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELLDLG
YNRIRSLARNVFAGMIRLKELHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSWTW
SSLQRLLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDWSISLNDISLAGNIWE
CSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLARALPKP
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVS
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYN
KSGSRECEV

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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FIGURE 537

GGGACTACAAGCCGCCCGCTGCCGTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGCCACCGCGAC
 TCCGGCTCTGCGCTCGGCTGCCTGACTCTTCCGTGCTGCTGCTTTCAAGGGCTGCCGTGATAGGGCTGTAATC
 TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGAACACTGTCTTCATCATACGGATTGCG
 AGACAAGTGACCCAGGATCGAGTGGAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAAA
 TTCAGGGAGACTTGGCGGGCTGTGAGGAAATTACTCGGGAGACATCCCTGAAGATCTGGATGAGATTGTGATCGAGTTAA
 ACTCAGCCCTTATCGCTGTGAGGCTGTGAGGAAATTGTGAGGAAATTGTGAGGATTGTGATCGAGTTAA
 CTGTGCAAGTGAAGCCAGTGACCCCTGTGCTGTAGAGTGACCGAAGGCTGTACCGTAGGCAAGATGGCAACACTGC
 ACTGCCAGGAGAGTGAGGGCACCCCCCGGCCACTACAGCTGTATCGCAATGATGTACACTGCCACCGGATT
 CCAGAGCCAATCCCAGATTTCGCAATTCTCTTCCACTTAAACTCTGAAACAGGCACTTGGTTCACTGCTG
 TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
 AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGTTCTGGTTGTCTGTACTGGCCCTGA
 TCACGTTGGGATCTGCTGTGCATACAGACGTGGTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA
 ACCCAGGGAAACAGATGGAGTTAACATACATCCGCACTGACGAGGAGGGCACTTCAGACACAAAGTCATCGTTG
 TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGACACATACCTCTGCTAGAAACTCTGTCAA
 GGCAGCAGAGCTGATGCACTCGGACAGAGCTAGACACTCATCAGAAGCTTCGTTGGCCAAGTGTGACCA
 CTACTCTTCTACTCTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
 GGAAGCAAAAGTGGGTGCGTTACTGAGTTGGGTTCTAATCTGTTCTGGCCTGATCCGCATGAGTATTAGG
 GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGCCCTGTGAAGCCAGCATGTTCAACACTGGTGT
 CAGCAGCCACGACAGCACCATGTGAGATGGCAGGGTGGCTGGACAGCACAGCAGCGCATCCGGGGAAACCCA
 GAAAAGGCTTCTACACAGCAGCCTACTTCATGGCCACAGACACCCACCGCAGTTCTTAAAGGCTCTGC
 TGATCGGTGTTGCACTGAGTTGGAGAAGCTTTGGATCAGCATTGTAACAAACCAAAATCAGGAAG
 GTAAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
 ACCTCGCTTCTAGGCTAACGCTGAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTATTTATAAAATT
 TACATCTAAATTGGTCAAGGATGTTGATTATTGAAAGAATTCTATTTAAACTGTAATATTGTTATTTGTT
 CATACAAATGTTAAATAACCTATTTTTAAAGGTTCAACTTAAGGTTAGAAGTCAAGCTACTAGTGTAAAT
 TGGAAATATCAATAATTAGAGTATTTCACCAAGGAACCTCTCATGGAAGTTACTGTGATGTTCTTTCT
 CACACAAGTTTACGCTTTTCACAAGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
 TAAAATTCCAGGTTAGCAATGTTGAAATCAGTTGATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
 GCCTCTCTGAGATGACTAGGACAGCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG
 CCAGTCAGCTCTGGGGTGCAGGGGCCAGGGCCCTCTAGCTCACTGTTGCCCGTGTCTGCCAGGAGGCC
 GCCATCCTTGGGCCCTGGCAGTGGCTGTGCTTACTCACGTGGCCCTGCTTCATCCAGCACAGC
 TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCCAGCTTGGGCTCTGTAACAGACCTCT
 TTTGGTTATGGATGGTCACAAAATAGGGCCCCAATGCTATTTTTTTAAGTTGTTAATTATTGTT
 AAGATTGTCAAGGCCAAGGCAATTGCGAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT
 CCCACTGTTCTCTTGCACAGAGAAAGCACCCAGCAGGCCACAGGCTCTGCGATTCAAAACAAACCATGAT
 GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGGCCAGGTGAAAGGCCCTGGGGGGAGGAAAG
 TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGGGGAGACACTGCTCCCT
 TGTGGGGGACATTAGCAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
 GCCGTCGCTGGCACTCAGGACTGAAGTGTGTAAGGAGGAGCTGTGAGAAGGAGCACTCCACTGTGCTGG
 GAATGGCTCTCACTCACCTGTGTTCTCAGCTTCAAGGAGGAGCTGTGAGAAGGAGCACTCCACTGTGCTGG
 AATTGCAATCATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCCTGGCAGAGGCA
 GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
 CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCACCCACCTCAGCGTTGGGATTACGCTCCAGCCTCCT
 TCTTGGTTGTCATAGTGTAGGGTAGCCTATTGCCCTCTTCTTATAACCTTAAACCTTCTACACTAGTGCCA
 TGGGAACCAAGGCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCATAACTGAGACTAGA
 CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
 GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
 CTCATTATAAAAGCTCAAAAAACCCA

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FIGURE 538

MALRRPPRLRLCARLPDFLFFFRLGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDP
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVVARNDRKEI
DEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR
FRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVV
LAVALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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FIGURE 539

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAGC
GCAACGGTGTGGTCCAAGCCGGGCTCTGCTTCGCCTCTAGGACATACACGGGACCCCCTAA
CTTCAGTCCCCAAACGCGCACCTCGAAGTCTTGAACTCCAGCCCCGACATCCACGCGCG
CACAGGCGCGGCAGGCAGGTCCGGCGAAGGCAGTCGCGCAGGGGGTCGGCAGCTGG
GCTCGGGCGGCGGGAGTAGGGCCGGCAGGGAGGGCAGGGAGGCTGCATATTCAAGAGTCGCGGG
CTGCGCCCTGGGAGAGGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCA**A**
TGAGCCGCGTGGTCTCGCTGCTGGCGCCGCGTGTGCTGCGGCCACGGAGCCTTCTGCC
GCCCGTGGTCAGCGGCCAAAGGTGTGTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG
CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTCAGGAGGCACGCCCTGGCTGTGAGAGTG
AGGGAGGAGTCTCCTCAGCCTTGAGAATGAAGCAGAACAGAACAGTTAATAGAGAGCATGTTGC
AAAACCTGACAAAACCCGGACAGGGATTCTGATGGTATTCTGGATAGGGCTTGGAGGA
ATGGAGATGGCAAACATCTGGTGCCTGCCAGATCTACCCAGTGGTCTGATGGAAGCAATT
CCCAGTACCGAAACTGGTACACAGATGAACCTCCTGCGGAAGTGAAAAGTGTGTTGATGT
ATCACCAACCAACTGCCAATCCTGGCCTGGGGTCCCTACCTTACCAAGTGGATGATGACA
GGTGTAACTGAAGCACAATTATATTGCAAGTATGAACCAGAGATTAAATCCAACAGCCCTG
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTACTGAAG
CAGGTATAATTCCAATCTAATTATGTTTACCAACAATACCCCTGCTCTACTGATAC
TGGTTGCTTGGAACCTGTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAAACTA
GTCCAAACCAGTCTACACTGTGGATTCAAAAGTACCAAGAAAAGTGGATGGAAGT**A**
ATAACTCATTGACTTGGTCCAGAATTGTAATTCTGGATCTGTATAAGGAATGGCATCAG
AACAAATAGCTTGGAAATGGCTGAAATCACAAGGATCTGCAAGATGAACGTGTAAGCTCCCT
TGAGGCAAATATTAAGTAATTCTTATATGCTATTATTCATTAAAGAATATGCTGTGCTA
ATAATGGAGTGGACATGCTTATTTGCTAAAGGATGCAACCAAACCTCAAACCTCAAGCAAA
TGAAATGGACAATGCAGATAAAGTGTATCAACACGTCGGGAGTATGTGTTAGAAGCAAT
TCCTTTATTCTTCACCTTCATAAGTGTATCTAGTCATGTAATGTATATTGTATTGA
AATTACAGTGTGCAAAGTATTACCTTGCATAAGTGTGATAAAAGTAAACTGTTCTA
ATATTATTTATGGCATCTCATTTCATAACATGCTTTGATTAAGAAACTTATTAC
TGTGTCACTGAATTCACACACACAAATATAGTACCATAGAAAAGTTGTTCTCGAA
ATAATTCACTTTCAGCTCTGCTTGGTCAATGTCTAGGAAATCTCTCAGAAATAAGA
AGCTATTCAATTAGTGTGATATAACCTCTCAAACATTACTTAGAGGCAAGGATTGTCT
AATTCAATTGTGCAAGACATGTGCCTTATAATTATTTAGCTAAACAGATTTG
TAATAATGTAACATTGTAATAGGTGCATAAACACTAATGCAGTCATTTGAACAAAAGAAGT
GACATACACAATATAAAATCATATGCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTG
AGGGTTCTGAAATCAATGTGGTCCCTCTTGCCTAAACAAAGATGGTGTGCGGGTT
GGGATTGACACTGGAGGGCAGATAGTGCAAAGTTAGTCTAAGGTTCCCTAGCTGTATTAGC
CTCTGACTATATTAGTATACAAAGAGGTATGTGGTTGAGACCAGGTGAATAGTCACATCAG
TGTGGAGACAAGCACAGCACAGACATTAGGAAGGAAAGGAACTACGAAATCGTGTGAAA
ATGGGTTGGAACCCATCAGTGCATATTCAATTGATGAGGGTTGCTTCAAGAGA
AAGTTGTAACCTCTGGTCTTCATATGTCCTGCTGCCCTTAAACAAATAAGAGTTCTG
TTCTGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 540

MSRVVSLLLGAALLCGHGFCCR VVSGQKVCFADFKHPCYK MAYFHELSSRVS FQE ARLACES
EGGVLLSLEN EA EQKLIESMLQNLTKPGTG ISDGDFWIGLWRNGDQTS GACP DLYQWSDGSN
SQYRNWYTDEPSCGSEKCVV MYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP
VEKP YLTNQPGDTHQN VVVTEAGIIPNLIYVVIPTIPLL LILVAFGTCCFQMLHKS KGRTKT
SPNQSTLWISKSTRKESGM EV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

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FIGURE 541

GGAGAAATGGGAGAGAGCAGTGAGAGTGGAGTCGGGGTCCGGTGGTCTGCTGCTGGCATGCCCTG
 CCACAGCCACTGGGCCCGAAGTTGCTCAGCTGAAGTAGACACCACCTGGTGTGCGAGGCCGGCAGGTGG
 GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTCTGGGCATTCCATTGCCACGCCACTGGGCCCTGACC
 GGTTCTCAGCCCCACACCCAGCACAGCCTGGGAGGGTGTGGGGATGCCAGCAGCACTGCCCCCCAATGTGCCCTAC
 AAGACGTGGAGAGCATGAACAGCAGCAGATTGCTCTCAACGGAAACAGCAGATCTCTCGTGGTACAGAGGACT
 GCCTGGTCTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTAGGCCGGTGTGGTACAGGATGGGTCCATG
 GAGGCCGCTCTGATAACTGGCGTCCACCTCCTACGATGGATCAGCTGGCTGCCATGGGATGTGGTGTGG
 TTACAGTCCAGTACCGCTTGGGCTCTTGGCTCTTCAGCAGCTGGAGATGAGCATGCCACCTGGCAACCAGGGCT
 TCCTAGATGTTGAGCTGCTTGCCTGGGTGCAAGAAAACATGCCCTTCGGGGTGACCTCAACTGTGTCA
 CTGTTCTGGTGGATCTGCCGGTGGAGCATCATCTGGCTGGTCTGGTCCAGGGCTGAGCTCAGGAGGCTGTTCC
 ACAGAGCCATCACAGAGTGGGGTCACTACCACCCAGGGATCATGACTCTCACCCGGCCCTAGCTCAGA
 AAATCGAAACACCTTGGCTGCAGCTCAGCTCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
 AAGAGCTGGTCTTAGCAAGAAGCTAAAAACTATCTATCCTCTCACCGTGTGGACTGTCTCCCCAAAA
 GCCCCAAGGAACCTCTGAAGGAGAACGCCCTCCACTCTGTGCCCTTCCTATGGGTGTCACAACACCAGGTTCA
 GCTGGCTCATCCCCAGGGCTGGGTCTGGATACAATGGAGCAGATGAGCCGGAGGACATGCTGGCATCT
 CAACACCCGCTTGACCAGTCTGGATGTGCCCTGAGATGATGCCACCGTCAAGATGAATACTAGGAAGCA
 ACTCGGACGCACAAGCAAATGCCAGGGCTCCAGGAATTCATGGGTGACGTATTCAATGTCCCACCGTCA
 GTTTTCAGATACTTCAGAGATTCTGGAAGGCCCTGTCTTTCTATGAGTTCCAGCATCGACCAGTTCTT
 CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGCCAGGGTGTCTGGTGTGAGGCTCTCTCA
 TGGACGAGAGCTCCGCTGGCTTCCAGGGCACAGAGGAGGAGAACAGCTAACGCTCACCAGTGGCC
 AGTGGACCCACTTGCCCGACAGGGGACCCAAATAGCAAGGCTCTGCCCTTGGCCCAATTCAACCAGGG
 ACAAAATCTGGAGATCAACCCAGTGCACAGGGCGACAGAACAGTGGAGGAGAACAGGAGGCTGGATGCA
 AGACGCTCCCCAGCAAGATAACAACAGTGGCACCAAGAACAGAACAGGAGGAGGACCTCTGA
 AGGCCTGAACCTCTGGCTGGGCAAAACACTCTCAAGTGGTGGAGCTCCAGGGCACACGGCAGCCCCTC
 CCCCTGCTGAGACTTAACTCCACCGCCCTAAAGTGTGGCCCTCTGTGACTGGAGTTATGCTCTT
 ATGTCACAAGGCCCTCCACCTGGGCATTGACAGTCTCCCTCTGGCTGAAGTGCCTTCTGCTT
 CTTCTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCAGGAAGCCTCCCTGCTT
 TGGCTGTGGCCCGAGTCTGCGTCATTAGAGCACAGTCCACCGAGGCTAGCACCGTGTGTGTCT
 CCCCTCAGAGGAGCTCTCAAAATGGGGATTAGCCTAACCCACTCTGTACCCACACCAGGATGGGTGG
 CCTGGAGCTAGGGGGTGTGCTGAGTGAGTGAAACACAGAATATGGGATGGCAGTGTGAACCTGAAC
 CCAGAGCCTCAGGTGCCAAAGCCATACTCAGGCCACCGACATTGTCACCCCTGGCAGAGGGTGCATGCC
 AATGGCAGAGACCTGGGATGGAGAACGCTGGGCCAGGGGATCCAGCCTAGAGCAGACCTAGCCCCTGAC
 TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCTCTGTGCTGCCAGTCTGGCCCTGCACAAGACAA
 CAGAATCCATCAGGGCCATGAGTGCACCCAGACCTGACCCCTACCAATTCCAGGCCCTGACCTCAGGAC
 CCAGCTCCCAGCCCCAGTGCCGGTCTCCCTCCCTGGCTGGGGAGACCAGTTCTGGGAGCTTCCAAG
 AGCACCCACCAAGACACAGCAGGACAGGCCAGGGAGGGCAGTGGACCAAGGGCATCCGTGGCTATTGT
 GAGAGAACAAAAGAGAACCCCCACTCGGGCTGCAAAGGTGAAAGCACCAGAGGTTTCAGATGGAG
 GTGACAGTGTGTGGCAGGCCCTACAGCCCTCGCTCTCCCTGCCCTCTGCTGGGCTCCACTTTGG
 GCACTGAGGAGCCCTCAACCCGCCCTGCACTGTAGGAGGCCCTTCTGGCTGGCCAAGGCCGGAG
 CCCTCAGCTGGGGAGGGTGGCGAGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 AGTGAAGTCTGG
 TAGCACCTGGGCCAGCAGCTGCTGTGCTGATTTCTGCTGGGCTTAGCTGCTGCCCTCCC
 GAGCTGAGGCCCTCATGCTGACCCCTCCCCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CGCCGCCCTGCTCCACAGGCCAGGCTGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CTGGCAGGCAGCTCCACCTGCTGCCCAAGTGTGGATCCACTGGGTGAAGGCCAGCTGGCT
 GGAGACTGGAGAACCTTATGCTAGCTAACGGATTGTAATACACCGATGGCACTCTGTAT
 TGTAACACACCAATCAGCACCCCTGTGTCTAGCTAGTGTGAATGCCAACACTCTGTATCTGG
 ACTCTGGTGGGACTTGGAGAACCTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGG
 ATGTGGAGAACCTTGTGCTAGCTAACGCCAACATAGCACCCCTGTCAAACAGACCA
 ACTTGACTCTGTGAAATGGGAGAACCTTGTGCTACTGCCACTGCTGAGGCCAG
 GGACCAATCAGCAGGATGTGGGTGGGGAGACAAGAGAAATAAAGCAGGCTGCTGAGGCCAG
 CCCTCGGGTCCCCCTCCACGCCGTGGAAGCTTGTCTTCGCTCTTGCAATAAATCT
 TGCTACTGCCAAAA

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FIGURE 542

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLGI
PFAQPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV
LNVYSPAEPAGSGRPVMVVHGGALITGAATSYDGSALAAYGDVVVTVQYRLGVLGFFSTG
DEHAPGNQGFLDVVAALRWVQENIAFPFGGDLNCVTVFCCSAGGSIISGLVLSPVAAGLFHRAI
TQSGVITTPGIIDSHPWPLAQKIANTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT
VDGTVFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDMLAISTPVL
TSLDVPPEMMPTVIDEYLGSNSDAQAKCQAFQEFGMDVFINVPTVSFSRYLRDSGSPVFFYEF
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEQLSLTMMAQWTHFA
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA
QEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 543

TGTGCCCTGGCCCTGCCATGCAGACCCCGCGAGCGTCCCCTCCC GCCCGGCCCTCTGCTTCGCTGCTGCTA
CTGGGGGGCGCCCCACGGCCTTTCTGAGGAGCCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC
TATCCCGTGTGTTGGCAGCGGGCCCGACGCCTGACCCCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTATTGGGGACAGGGAACCTCTACCGCGTAGAGCTGGAGCAGCGA
TCCACGGAGCTGCGGTACAGAGGAAGCTGACCTGGAGATCTAACCCCAGCGACATAAACGTGTGTCGGATGAAG
GGCAAACAGGAGGGCGAGTGCGAAACTCTGTAAGGCTGCTGCTCCCTGGGACGAGTCCACGCTTTGTGTC
GGTTCCAACGCCTCAACCCGGTGTGCGCAACTACAGCATAGACACCCCTGAGCCCCCTCGAGAGACAACATCAGC
GGTATGGCCCGTGGCCCTGACGACCCAAAGCAGCGCATGTTGCCCTCTTCTCTGACGGGATGCTCTCACAGCT
ACTGTACCGACTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTGGGGACAGGGCCACCCCTGCGCACCGTG
AAACATGACTCCAAGTGGTCAAAAGAGCCTTACTTGTCCATGCGGTGGAGTGGGGCAGCCATGCTACTTCTC
TTCCGGAGATTGCGATGGAGTTAACTACCTGGAGAAGGTGGTGTGCCCCGAGTGTGCAAGAAC
GACGTGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCTTCCCTGAAGGCGGGCTCAACTGCTCTGTA
CCCAGGAGACTCCCATTCTACTCAACGTGTCAGGCTGTCAGGGCGTGGTCAGCCTGGGGCCGGCCCGTG
GTCCTGGCGTTTCCACGCCCAGCAACAGCATTCCGGCTGCTGCGCTGCGCCCTTGACCTGACACAGGTG
GCAGCTGTGTTGAAGGCCGTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGGCGAGGATCAG
GTGCTCGACCCCGGGGGTGTGCGCAGCCCCGGGATGCAAGTACAATGCCCTCAGCGCTTGCGGATGAC
ATCCTCAACTTGTCAAGACCCACCCCTGATGGACGAGGCGTGCCCTCGCTGGGCATGCGCCCTGGATCCTG
CGGACCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGAGCCGGCCCTGGGCACCAAGACCGTT
GTCTTCTGGGTTCTGAGGCGGGACGGTCTCAAGTTCTCGTCCGGCCAAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTCCTGGAGGAGTTGAGACCTACCGGCCGACAGGTGTGGACGCCGGCGTGGCGAGACA
GGGCAAGCGGCTGAGCTGGAGCTGACGCACTCGGGGGCTGCTGGCTGCCCTCCCCCGTGGCTGGTC
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGATGAAAGAACTGTATCGGCACTCAGGACCGTCT
GGGTGGGCCCCCAGCGCTCTGCATCTCCCTCAGCCGGGCAACAGGAGCCCTTGGACGCCGGTGGCGAGGACA
GCCAGCACCTCAGGCTTAAGGGACTGCAACAGGACTCTGGGGCCAGCAGCTCTCCGAGGAGGCCGGTGGTG
TCGGTGAACCTGCTGGTAACCTGCTGGTGGGGCCCTTCGTGGTGGAGCCGTGGTGTCCGGCTCAGCGTGGC
TGGTCTGCCCCCTCGTGAAGCGCGGGAGCTGGGCCGGCGCAAGGACAAGGAGGCCATCTGGCGCACGGGCG
GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGCGAGCGCAGGGCGCAGGGTCCGGGGCGGGGGGGAGGCGGT
GGCGGTGGCGCCGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAAGACGGCTGGGCCAAGGCCACGCTG
CTGAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCGAGCAGGCCGCTGCCAGAAGCGC
CTGCCCACTCCGACCCGACCCCCACGCCCTGGGCCCGGCCCTGGGACCAAGGCCACCCCTGCTCCGGCC
TCCGCTTCATCCTCCCTCTGCTGCTGGCGCCGCCGGGCCCGAGCAGCCCCCGGCCCTGGGAGGCCAC
CCCGACGGCCGCTCTATGCTGCCCGGCCGCCCTCCACGGCAGCTCCGCTCACCCCCCACGCCAGC
CCGGACCGCCGGGGTGGTGTCCGCGCCACGGGCCCTTGACCCAGCCTCAGGCCGATGCCCTCCCG
CCCTGGAGGCCGCCCGACGGCAGCCTGAGGAGGCCACTGGGCCACGCCCTCCGGCCGCCACCCCTGCC
CGCACCCACACGTTCAACAGCGCGAGGCCCTGGGACCGCCACGCCGGCTGCCACGCCGGGCCACA
GACTTGGCCACCTCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTCCCTTAGGCCGGGGCCCCCG
ATGCCCTGGCAGTGCCAGCCACGGGAACCCAGGAGCGAGACAGGTGCCAGAACGCCGGGGCCGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGGGAGTGGGGGGCCCCCTCCGGCCACAAGGAAGGCCACAAACAG
CTCGCCCTCCCCCTACCGGGGCCGAGGACGCTGAGACGGTTGGGGTGGGGGGAGGACTTTGCTATG
GATTGAGGGTGAACCTTATGCGCGTAGGTTGGGTTTTTGTGAGTGGTTCTTGTGCGTTTCTTAAC
AATTGCAACACTCCGTTCTCGGGGTTGGCGAGGCCAGGGAGGCTTGGACGCCGGTGGGAATGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCAACCCAGGCCCTGGCGTGTGGGTGTGCG
TGCCTGCGTGTGCGTGTGCAAGTGGCCACCGCGTGCAGGGTGTGTCACGAGCGACGATCGTGGTGGGCCAGCGGCC
TGGCGCTGGCTGAGCCGACGCTGGGGCTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGGTGGGAATGGAGTTGAAC
CCCCCCCACCTCGCAGAGGGAAAGCAGGGACAATGCCGGGTTCAAGGAGGAGACAGCAGAGGAGGCCCTGCCGG
AGTCACATCGGCAGCAGCTGCTAAAGGGCTGGGGCTGGGGGCCAGGGAGGTGGGTGGGGCCCTCTGAA
ATACGGCCCCAGGGTGGTGAAGAGAGTCCCATGCCACCCGCTCCCTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTGGAGTTGCCCTCCCCAGCCCCCTCCCCATCAAT
AAAACCTGTTACAACCAAAAAAAAAAAAAAA

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FIGURE 544

MQTPRASPPRPALLLLLLLGGAHGLFPEEPPLSVAPRDYLNHYPVFGSGPGRLTPAEGAD
DLNIQRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINCRMKGKQEGEC
RNFKVLLLRLDESTLFVCGSNAFPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREIAMEF
NYLEKVVVSVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGVVSLG
GRPVVLAVFSTPSNSIPGSACAFDLTQVAVFEGRFREQKSPEIWTVPEDQVPRPRPGCC
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQQLTRAVDVAGPWGN
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFEEFETYRPDRCGRPGGGETGQRLLSLELD
AASGGLLAAFPRCVVVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTTRAAFEQDV
SGASTSGLGDC TGLLRASLSEDRAGLVSVNLLVTSSVAFFVVGAVVSGFSVGFWFVGLRERREL
ARRKDKEAILAHGAGEAVLSVSRLGERAQGPGRGGGGGGAGVPPEALLAPLMQNGWAKAT
LLQGGPHDLSGLLPTPEQTPLPKRLPTPHPHHALGPRAWDHGHPLL PASASSLLLAPA
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRVVSAPTGPLDPASAADGLPR
PWSPPPPTGSLRRPLGPHAPPAATLRRHTFNSGEARPGDRHRGCHARPGTDLAHLLPYGGADR
TAPPVP

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

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FIGURE 545

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCGATTTCTCCCCAGTTCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTCGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTGACATTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTCACGGGAG
GCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCTTCAGCCTCTCTGCTGCGTTTATCTCCTATGGACTCCTCACTGGACTGAAG
ACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATGGATTTCT
GAGATACGGGCAGTGTGCAAGCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTGCCATTGCTAAGACTC
TATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACA
TGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTCTGCAATGGATGGAG
GAGACAGAATAGGAGGAAAGTGTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCAAACCACCATCTTTACTGTACTAGTCTTGCT
GGTCACAGTGTATCTTATTATGCATTACTGCTTCTGCATGATTGCTTATGCATCCCC
AATCTTAATTGAGACCATACTTGATAAGATTTGTAATATCTTCTGCTATTGGATATATT
TATTAGTTAATATATTATTATTGCTATTAAATGTATTATTTTACTGGACATG
AAACTTAAAAAAATTCACAGATTATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT
ACAGTAAAAAAAAACCTTGAAATTCTAGAAGAGTGGCTAGGGGGTTATTCAATTGTAT
TCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGATATTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATTGCACATCTACCTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGATCTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTCTACAAATAAGTTTCTGCATACCAAAAAAAAAAAAAAA

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FIGURE 546

MRQFPKTSFDISPEMSFSIYSLQPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPE
IFSSREAWQFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLRHLLRLYLDRVFKNYQTPDHY
TLRKISSLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI
LLQWMEETE

Important features:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 547

AGCAACTCAAGTTCATCATTGTCTTGAGAGAGAGGGAGCAGCGCGTTCTGGCCGGGACAGCA
GAACGCCAGGGGACCCTCACCTGGCGCGCCGGGCACGGGCTTGATTGTCTGGGTCGCG
GAGACCCCGCGCGCTGCCCTGCACGCCGGCGAACCTTGAGTCGCGTGGCTGCTGCGA
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTCTGTCCACCTCTTACACTCTTCATTT
ATCGGTGGATCATTCGAGAGTCCGTCTTGTAAATGTTGGCACTTGCTACTTTATTGCTTC
TTTCTGGCGACAGTTCCAGCACTGCCGAGACCGGGAGAAAGGCAGCTGAGCCCAGAAG
AGCGAAATATGGGGACCCGGCTAAAAGCAGACGTCGTCCTTCCCAGGCTATTTCTATATT
CAGGCAGTGGATACTCAGGGAATAAATTCACATCTCCAGGCAGGTTAGACCGAAAAGAT
GGGTCTTCATAGTAAGATAACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGAAATTAAA
TTCCAAGGGCAACATGTGGCAAATCCCCATATATTTAAAAGGGCGGTTACCATGAGAAC
TGTGACTGTCTCTGCAAGATACTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT
GCTCAGATTCAAGAGAGATCTGGCACATTCCCTGCTGTGGATCCAGAAAAGATTGCACTAGAA
ATCCCAAAAAGATTGGACAGAGGAGCAGGCCATGTCACTACACCTTAAAGGATAACAAGGTT
TATATCAAGACTCATGGTGAACATGTAGGTTTAGAATTTCATGGATGCCATACTACTTCT
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTTTGTTAATTGGAGACTGGCCTTG
GAAAAAAAGAAATCCAATTCAAACATCCATCCGATTTCTGGTGTGGCTCCACAGATTCC
AAGGATATCGTATGCCTACGTACGATTGACTGATTCTGTTCTGGAAACCATTGGCCGGTA
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGCTCCCTGGAAAGCAAAAATTCCACT
GCCGTCGGAGAGGGCGAGACAGCCGAAAGAGAGACTCGAGCTGGTAAACTCAGTAGAAAA
CACCCAGAACTCATAGACGCTGTTACCAACTTTCTTAAACACGATGAAAACCTG
TATGGTCCCATTGTGAAACATATTCATTTGATTCTTCAAGCATAAGTATCAAATAAAT
ATCGATGGCACTGTAGCAGCTTATGCCCTGCCATATTGCTAGTTGGTGCAGTGTTGCTG
AAGCAGGATTCCATCTACTATGAACATTTACAATGAGCTGCAGCCCTGGAAACACTACATT
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACTTAAATGGCGAAAGATCACGATGAA
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTGCAAGAAATACTCATGGCGATGAC
ATATTCTGTTATTATTCAAAACCTTCCAGGAATATGCCAATTACAAGTGAGTGAGCCCAA
ATCCGAGAGGGCATGAAAAGGGTAGAACACAGACTGAGGACGACCTTCCCTGTACTTGC
CATAGGAAAAAGACCAAAAGATGAACTTGATATGCAAAATAACTCTATTAGAATAATGGTGC
TCTGAAGACTCTCTTAACTAAAAAGAAGAATTTTAAGTATTAATTCCATGGACAATATA
AAATCTGTGTGATTGTTGCAGTATGAAGACACATTCTACTTATGCACTATTCTCATGACTG
TACTTTAAAGTACATTTAGAATTATAATAAAACCACCTTATTTAAAGGAAAAAAA

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FIGURE 548

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPARFYIQAVDTSGNKFT
SSPGEKVFQVKVSAPEEQFTRGVQVLDRKDGSIIVRYRMYASYKNLKVEIKFQGQHVAKS
ILKGPVYHENCDCPLQDSAALREMNCPETIAQIQRDLAHFPADPEKIAVEIPKRGQRQSL
CHYTLKDNYIKTHGEHVGFRIFMDAILLSLTKVKMPDVELFVNLDWPLEKKKSNSNIHP
IFSWCGSTDSDKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE
RLELVKLSRKHPELIDAFTNFFFKHDENLYGPIVKHISFFDFFKHYQINIDGTVAAYRLP
YLLVGDSVVLQDSIYYEFYNELOPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKKIAKAGQE
FARNNLMGDDIFCYYFKLFQEYANLQVSEPOIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

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FIGURE 549

GGGTGATTGAAC TAAAC CTTGCCGCACCGAGTTGCAGTACGGCGTCACCCGACCGCTGC
CTGCTTGC GGGTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTATAGTGGC
GTGGCCGAGGCCGGGTGACCCTGCCGGAGCCTCCGTGCCAGCGACATGTTCAAGGTAATT
AGAGGTCCGTGGGCCAGCCAGCCTGAGCTTGCTCACCTCAAAGTCTATGCAGCACCAAAA
AGGACTCACCTCCAAAAATTCCGTGAAGGTTGATGAGCTTCACTCTACTCAGTTCCGTGAGG
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTGAAGAAAGCATCTCACAGCTCCGAC
ACTATTGCGAGCCATACACAACCTGGTGTCAAGAACGTACTCCAAACTAAGCCCAAGATGC
AAAGTTGGTTCAATGGGGTTAGACAGCTATGACTATCTCCAAATGCACCTCCTGGATTT
TTCCGAGACTGGTGTATTGGTTTGCTGGCCTTATTGGACTCCTTGCTAGAGGTTCAA
AAATAAAGAAGCTAGTGTATCCGCCTGGTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC
AACAAAGCCATCGTGTTCGCCAGGTCAAGTGGGGAGAGATTATATGACTGGGGTTACGAGGAT
ATATAGTCATAGAAGATTGTGAAGGAGAACTTCAAAAGCCAGGAAATGTGAAGAATTAC
CTGGAACTAAGTAGAAACTCCATGCTGCCATCTTAATCAGTTAGGTAAACATTGGAAA
CTCCATAGAATAAATCAGTATTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATT
AATTGGCTTCTCTCAGGAAAAACTAGACCAGACCTCTGTTATCTCTGTGAAATCATCCT
ACAAGCAAACTAACCTGGAATCCCTCACCTAGAGATAATGTACAAGCCTAGAACTCCTCAT
TCTCATGTTGCTATTATGTACCTAATTAAAACCAAGTTAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

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FIGURE 550

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPPEGQSKYVEEARSQLLEES
ISQLRHYPCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFPRLGIVIGFAGLIGLL
LARGSKIKKLVYPPGMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG
NVKNSPGTK

Important features:

Signal peptide:

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
7 June 2001 (07.06.2001)

PCT

(10) International Publication Number
WO 01/40466 A3

| | | |
|---|--|--|
| (51) International Patent Classification ⁷ : | C12N 15/12, C07K 14/47, 14/705, C12N 15/62, C07K 16/18, 16/28, G01N 33/53, A61K 38/17, C12Q 1/68 | PCT/US99/30911 20 December 1999 (20.12.1999) US |
| (21) International Application Number: | PCT/US00/32678 | PCT/US99/31243 20 December 1999 (20.12.1999) US |
| (22) International Filing Date: | 1 December 2000 (01.12.2000) | PCT/US99/31274 30 December 1999 (30.12.1999) US |
| (25) Filing Language: | English | PCT/US00/00219 5 January 2000 (05.01.2000) US |
| (26) Publication Language: | English | PCT/US00/00277 6 January 2000 (06.01.2000) US |
| (30) Priority Data: | | PCT/US00/03565 6 January 2000 (06.01.2000) US |
| | PCT/US99/28301 1 December 1999 (01.12.1999) US | PCT/US00/04341 11 February 2000 (11.02.2000) US |
| | PCT/US99/28634 1 December 1999 (01.12.1999) US | PCT/US00/04342 18 February 2000 (18.02.2000) US |
| | PCT/US99/28551 2 December 1999 (02.12.1999) US | PCT/US00/04414 18 February 2000 (18.02.2000) US |
| | PCT/US99/28564 2 December 1999 (02.12.1999) US | PCT/US00/04914 22 February 2000 (22.02.2000) US |
| | PCT/US99/28565 2 December 1999 (02.12.1999) US | PCT/US00/05004 24 February 2000 (24.02.2000) US |
| | 60/170,262 9 December 1999 (09.12.1999) US | PCT/US00/05601 24 February 2000 (24.02.2000) US |
| | PCT/US99/30095 16 December 1999 (16.12.1999) US | PCT/US00/05841 1 March 2000 (01.03.2000) US |
| | | PCT/US00/05841 2 March 2000 (02.03.2000) US |

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

MSTMFA DTLLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQS KKKETITESAGR
QQKKKIERQE EKLKNNNRDL SMVRMKS MFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQ
GLSHRNLLGDDTTDCSF IFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPSGKFS

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 103-109, 163-169

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 53-57

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

WO 01/40466 A3



| | | | |
|----------------|--------------------------------|----|--|
| 60/187,202 | 3 March 2000 (03.03.2000) | US | (US). SHERWOOD, Steven [US/US]: 995 Lundy Lane, Los Altos, CA 94024 (US). SMITH, Victoria [AU/US]: 19 Dwight Road, Burlingame, CA 94010 (US). STEWART, Timothy, A. [US/US]: 465 Douglass Street, San Francisco, CA 94114 (US). TUMAS, Daniel [US/US]: 3 Rae Avenue, Orinda, CA 94563 (US). WATANABE, Colin, K. [US/US]: 128 Corliss Drive, Moraga, CA 94556 (US). WOOD, William, I. [US/US]: 35 Southdown Court, Hillsborough, CA 94010 (US). ZHANG, Zemin [CN/US]: 876 Taurus Drive, Foster City, CA 94404 (US). |
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| PCT/US00/15264 | 2 June 2000 (02.06.2000) | US | |
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| PCT/US00/22031 | 11 August 2000 (11.08.2000) | US | |
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| 60/000,000 | 15 September 2000 (15.09.2000) | US | |
| PCT/US00/30952 | | | |
| | 8 November 2000 (08.11.2000) | US | |
| PCT/US00/30873 | | | |
| | 10 November 2000 (10.11.2000) | US | |

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(74) **Agents:** **KRESNAK, Mark, T.** et al.: Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(81) **Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report*

(88) **Date of publication of the international search report:** 10 May 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/32678

| A. CLASSIFICATION OF SUBJECT MATTER | | C07K14/47 | C07K14/705 | C12N15/62 | C07K16/18 |
|-------------------------------------|------------------------|-----------|------------|-----------|-----------|
| IPC 7 | C12N15/12 C07K16/28 | G01N33/53 | A61K38/17 | C12Q1/68 | |

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|----------|---|-----------------------|
| X | WO 98 21328 A (KATO SEISHI ;PROTEGENE INC (JP); SEKINE SHINGO (JP); SAGAMI CHEM R) 22 May 1998 (1998-05-22) * see seq.ID's.12, 37 and 62: clone HP10122 * --- WO 99 09061 A (GENETICS INST) 25 February 1999 (1999-02-25) * see clone am910_li * | 1-20, 69-71 |
| X | --- | 1-20 -/- |

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

8 August 2001

Date of mailing of the international search report

12.11.01

Name and mailing address of the ISA
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Fax: (+31-70) 340-3016

Authorized officer

Smalt, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/32678

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|----------|---|-----------------------|
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| A | WO 97 07198 A (GENETICS INST) 27 February 1997 (1997-02-27) the whole document --- | |
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| P,X | WO 00 37630 A (GENETICS INST) 29 June 2000 (2000-06-29) * see clone AM910_1i * ----- | 1-13, 17-20 |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/32678

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 and 69-71, all partially

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 and 69-71, all partially

PR0177: nucleic acid with seq.ID.1, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.2 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.2 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide.

Inventions 2-242: claims 1-20 and 69-71, all partially

Subject matter as defined for invention 1, but related to the respective nucleic acid/polypeptide sequences of:

Invention 2: PR03574, represented by seq.ID.s 3 and 4,

Invention 3: PR01280, represented by seq.ID.s 5 and 6,

Invention 4: PR04984, represented by seq.ID's 7 and 8,

...
Invention 15: PR01471, represented by seq.ID.s 29 and 30,
(PR01114 skipped; follows below)

Invention 16: PR01076, represented by seq.ID.s 33 and 34, ...

Invention 92: PR04345, represented by seq.ID.s 185 and 186,
(PR04978 skipped; follows below)

Invention 93: PR04327, represented by seq.ID.s 221 and 222,

...
Invention 107: PR06028, represented by seq.ID.s 217 and 218,
(PR0100 skipped; follows below)

Invention 108: PR04327, represented by seq.ID.s 221 and 222,

...
Invention 132: PR0197, represented by seq.ID.s 269 and 270,
(PR0195 skipped; follows below)

Invention 133: PR0187, represented by seq.ID.s 273 and 274,
(PR0182 skipped; follows below)

Invention 134: PR0188, represented by seq.ID.s 277 and 278,

...
Invention 136: PR0184, represented by seq.ID.s 281 and 282,
(PR0185 skipped; follows below)

Invention 137: PR0200, represented by seq.ID.s 285 and 286,
(PR0202 skipped; follows below)

Invention 138: PR0214, represented by seq.ID.s 289 and 290,
(PR0215 skipped; follows below)

Invention 139: PR0219, represented by seq.ID.s 293 and 294,
(PR0211 skipped; follows below)

Invention 140: PR0220, represented by seq.ID.s 297 and 298,
(PR0366, PR0216, PR0221 skipped; follows below)

Invention 141: PR0228, represented by seq.ID.s 305 and 306,

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(PR0217, PR0222, PR0224 skipped: follows below)
Invention 142: PR0230, represented by seq.ID.s 313 and 314,
(PR0198 skipped: follows below)
Invention 143: PR0226, represented by seq.ID.s 317 and 318,
...
Invention 151: PR0323, represented by seq.ID.s 333 and 334,
(PR0245 skipped: follows below)
Invention 152: PR0246, represented by seq.ID.s 337 and 338,
...
Invention 155: PR0257, represented by seq.ID.s 343 and 344,
(PR0172 skipped: follows below)
Invention 156: PR0258, represented by seq.ID.s 347 and 348,
(PR0265 skipped: follows below)
Invention 157: PR0326, represented by seq.ID.s 351 and 352,
(PR0266 skipped: follows below)
Invention 158: PR0269, represented by seq.ID.s 355 and 356,
...

Invention 160: PR0328, represented by seq.ID.s 359 and 360,
(PR0344 skipped: follows below)
Invention 161: PR0272, represented by seq.ID.s 363 and 364,
(PR0301 skipped: follows below)
Invention 162: PR0331, represented by seq.ID.s 367 and 368,
...
Invention 165: PR0310, represented by seq.ID.s 373 and 374,
(PR0337 skipped: follows below)
Invention 166: PR0346, represented by seq.ID.s 377 and 378,
Invention 167: PR0350, represented by seq.ID.s 379 and 380,
(PR0526 skipped: follows below)
Invention 168: PR0381, represented by seq.ID.s 383 and 384,
...
Invention 173: PR0731, represented by seq.ID.s 393 and 394,
(PR0322 skipped: follows below)
Invention 174: PR0536, represented by seq.ID.s 397 and 398,
(PR0719 skipped: follows below)
Invention 175: PR0619, represented by seq.ID.s 401 and 402,
...
Invention 214: PR01475, represented by seq.ID.s 479 and 480,
(PR01312 skipped: follows below)
Invention 215: PR01308, represented by seq.ID.s 483 and 484,
...
Invention 222: PR01358, represented by seq.ID.s 497 and 498,
(PR01286 skipped: follows below)
Invention 223: PR01294, represented by seq.ID.s 501 and 502,
Invention 224: PR01273, represented by seq.ID.s 503 and 504,
(PR01279 skipped: follows below)
Invention 225: PR01195, represented by seq.ID.s 507 and 508,
Invention 226: PR01271, represented by seq.ID.s 509 and 510,
(PR01338, PR01343 skipped: follows below)
Invention 227: PR01434, represented by seq.ID.s 513 and 514,
...
Invention 237: PR01693, represented by seq.ID.s 536 and 537,

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(PRO1868 skipped: follows below)

Invention 238: PRO1890, represented by seq.ID.s 539 and 540,

...

Invention 240: PRO4353, represented by seq.ID.s 543 and 544,

(PRO1801 skipped: follows below)

Invention 241: PRO4357, represented by seq.ID.s 547 and 548,

Invention 242: PRO4302, represented by seq.ID.s 549 and 550.

For the sake of conciseness, the first subject matter is explicitly defined, the subject matter of inventions 2-241 are defined by analogy thereto, whereby the numbering of the sequences is followed, except for sequences which are mentioned in one of claims 21-68; inventions relating thereto follow below.

Invention 243: claims 43-49, 53, 54 completely,
and claims 1-24, 29-31, 35, 36, 69-71,
all partially

PRO1114: nucleic acid with seq.ID.31, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.32 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.32 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO1801 and/or PRO100 using their interactions with PRO1114, method for linking a bioactive molecule to a cell expressing PRO1801 and/or PRO100 through the use of PRO1114, and method of modulating at least one activity of said cell thereby.

Invention 244: claims 1-24, 29-31, 35, 36, 53, 54,
69-71, all partially

PRO4978: nucleic acid with seq.ID.187, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.188 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.188 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO1801 using its interaction with PRO4978, method for linking a bioactive molecule to a cell expressing PRO1801 through the use of

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

PRO4978, and method of modulating at least one activity of said cell thereby.

Invention 245: claims 39-42, 50-52, 55,
56 completely, and claims 1-20, 69-71,
all partially

PRO100: nucleic acid with seq.ID.219, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.220 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.220 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO1801 and/or PRO1114 using their interactions with PRO100, method for linking a bioactive molecule to a cell expressing PRO1801 and/or PRO1114 through the use of PRO100, and method of modulating at least one activity of said cell thereby.

Invention 246: claims 1-20, 57, 69-71,
all partially

PRO195: nucleic acid with seq.ID.271, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.272 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.272 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO195 protein.

Invention 247: claim 66 completely,
and claims 1-20, 58, 59, 69-71, all partially

PRO182: nucleic acid with seq.ID.275, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.276 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.276 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of

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said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for inhibiting the binding of A-peptide to factor VIIA using the PRO182 protein.

Invention 248: claims 1-20, 67, 69-71,
all partially

PRO185: nucleic acid with seq.ID.283, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.284 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.284 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for inhibiting the differentiation of adipocytes using the PRO185 protein.

Invention 249: claims 1-20, 57, 59, 60, 69-71,
all partially

PRO202: nucleic acid with seq.ID.287, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.288 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.288 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for stimulating the proliferation or differentiation of chondrocytes, and method for modulating the uptake of glucose or FFA by adipocytes using the PRO202 protein.

Invention 250: claims 1-20, 57, 69-71,
all partially

PRO215: nucleic acid with seq.ID.291, encoding a polypeptide comprising the amino acid sequence as represented in

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seq.ID.292 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.292 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0215 protein.

Invention 251: claims 1-20, 60, 69-71,
all partially

PR0211: nucleic acid with seq.ID.295, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.296 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.296 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by adipocytes using the PR0211 protein.

Invention 252: claim 61 completely,
and claims 1-20, 58, 59, 69-71, all partially

PR0366: nucleic acid with seq.ID.299, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.300 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.300 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for stimulating the proliferation of gene expression in pericytes using the PR0366 protein.

Invention 253: claim 62 completely,
and claims 1-20, 69-71, all partially

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PRO216: nucleic acid with seq.ID.301, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.302 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.302 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of proteoglycans from cartilage using the PRO216 protein.

Invention 254: claims 1-20, 57, 69-71,
all partially

PRO221: nucleic acid with seq.ID.303, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.304 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.304 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO221 protein.

Invention 255: claims 1-20, 69-71, all partially

PRO217: nucleic acid with seq.ID.307, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.308 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.308 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO217 protein.

Invention 256: claim 68 completely,
and claims 1-20, 69-71, all partially

PRO222: nucleic acid with seq.ID.309, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.310 or a nucleic acid having at least 80% homology

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thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.310 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for stimulating the proliferation of endothelial cells using the PR0222 protein.

Invention 257: claims 1-20, 59, 69-71,
all partially

PR0224: nucleic acid with seq.ID.311, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.312 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.312 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for stimulating the proliferation or differentiation of chondrocytes using the PR0224 protein.

Invention 258: claims 1-20, 57-59, 67, 69-71,
all partially

PR0198: nucleic acid with seq.ID.315, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.316 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.316 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for inhibiting the differentiation of adipocytes using the PR0198 protein.

Invention 259: claims 1-20, 57, 69-71,

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

all partially

PRO245: nucleic acid with seq.ID.335, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.336 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.336 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO245 protein.

Invention 260: claim 63 completely,
and claims 1-20, 57-59 69-71, all partially

PRO172: nucleic acid with seq.ID.345, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.346 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.346 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for stimulating the proliferation of inner ear utricular supporting cells using the PRO172 protein.

Invention 261: claims 1-20, 57, 69-71,
all partially

PRO265: nucleic acid with seq.ID.349, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.350 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.350 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO265 protein.

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Invention 262: claims 1-20, 57, 69-71,
all partially

PRO266: nucleic acid with seq.ID.353, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.354 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.354 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO266 protein.

Invention 263: claim 64 completely,
and claims 1-20, 57, 60, 69-71, all partially

PRO344: nucleic acid with seq.ID.361, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.362 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.362 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by adipocytes, and method for stimulating the proliferation of T-lymphocytes using the PRO344 protein.

Invention 264: claims 1-20, 59, 69-71,
all partially

PRO301: nucleic acid with seq.ID.365, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.366 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.366 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation

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or differentiation of chondrocytes using the PRO301 protein.

Invention 265: claims 1-20, 57, 69-71,
all partially

PRO337: nucleic acid with seq.ID.375, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.376 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.376 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO337 protein.

Invention 266: claims 1-20, 65, 69-71,
all partially

PRO526: nucleic acid with seq.ID.381, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.382 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.382 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of a cytokine from PBMC cells using the PRO526 protein.

Invention 267: claims 1-20, 57, 69-71,
all partially

PRO322: nucleic acid with seq.ID.395, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.396 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.396 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO322 protein.

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Invention 268: claims 1-20, 58, 69-71,
all partially

PRO719: nucleic acid with seq.ID.399, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.400 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.400 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells using the PRO719 protein.

Invention 269: claims 1-20, 59, 69-71,
all partially

PRO1312: nucleic acid with seq.ID.481, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.482 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.482 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation or differentiation of chondrocytes using the PRO1312 protein.

. Invention 270: claims 1-20, 57, 69-71,
all partially

PRO1286: nucleic acid with seq.ID.499, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.501 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.501 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO1286 protein.

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Invention 271: claims 1-20, 57, 69-71,
all partially

PRO1279: nucleic acid with seq.ID.505, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.506 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.506 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO1279 protein.

Invention 272: claims 1-20, 57, 60, 69-71,
all partially

PRO1338: nucleic acid with seq.ID.511, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.512 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.512 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for modulating the uptake of glucose or FFA by adipocytes using the PRO1338 protein.

Invention 273: claims 1-20, 57, 65, 69-71,
all partially

PRO1343: nucleic acid with seq.ID.513, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.514 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.514 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of

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TNF-alpha from human blood, and method for stimulating the release of a cytokine from PBMC cells using the PRO1343 protein.

Invention 274: claims 1-20, 59, 69-71,
all partially

PRO1868: nucleic acid with seq.ID.537, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.538 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.538 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation or differentiation of chondrocytes using the PRO1868 protein.

Invention 275: claims 25-28, 32-34, 37,
38 completely, and claims 1-20, 69-71,
all partially

PRO1801: nucleic acid with seq.ID.545, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.546 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.546 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO1114 and/or PRO4978 using its interaction with PRO1801, method for linking a bioactive molecule to a cell expressing PRO4978 and/or PRO1114 through the use of PRO1801, and method of modulating at least one activity of said cell thereby.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int'l Application No

PCT/US 00/32678

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